

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: April 3, 2006, 08:02:30 ; Search time 81 Seconds  
(without alignments)  
86.791 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980e:.\*  
2: geneseqp1980e:.\*  
3: geneseqp2000e:.\*  
4: geneseqp2000e:.\*  
5: geneseqp2002e:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004e:.\*  
9: geneseqp2005e:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	2	AAV43191 Schizophr
2	78	86.7	16	2	AAV43204 Schizophr
3	78	86.7	17	2	AAV43198 Schizophr
4	78	86.7	17	2	AAV43197 Schizophr
5	74	82.2	458	6	AAV43197 Carbohydr
6	74	82.2	458	8	ADQ30526 Pancreas
7	74	82.2	458	9	ADQ30526 Pancreas
8	65	72.2	16	2	AAV43202 Schizophr
9	65	72.2	17	2	AAV43196 Schizophr
10	65	72.2	18	2	AAV43195 Schizophr
11	65	72.2	19	2	AAV43194 Schizophr
12	65	72.2	20	2	AAV43193 Schizophr
13	65	72.2	28	2	AAV43192 Schizophr
14	65	72.2	50	8	ADU78952 Human pro
15	65	72.2	156	8	ADU78952 Human pro
16	65	72.2	269	6	ADU78952 Human pro
17	65	72.2	269	6	ADU78952 Human pro
18	65	72.2	272	6	ABU04378 Human exp
19	65	72.2	272	6	ABU04378 Human exp
20	65	72.2	336	6	ABU04376 Human exp
21	65	72.2	420	6	AAE38225 Human enz
22	65	72.2	429	6	ABU03958 Human exp
23	65	72.2	429	6	ABU03958 Human exp
24	65	72.2	433	2	AAW14001 Enolase p

25	65	72.2	433	2	AAW54357 Alpha Eno
26	65	72.2	433	6	ABU03944 Human exp
27	65	72.2	433	6	ABU03942 Human exp
28	65	72.2	433	8	ADQ30574 Pancreas
29	65	72.2	434	5	ABBS57379 Rat mucoc
30	65	72.2	434	5	ABPE5147 Hypoxia-r
31	65	72.2	434	5	ABPE5155 Hypoxia-r
32	65	72.2	434	5	AAW48922 Human eno
33	65	72.2	434	6	ABR64211 Angiogene
34	65	72.2	434	6	ABR64211 Angiogene
35	65	72.2	434	6	ABR59704 Human eno
36	65	72.2	434	6	ABU03929 Human exp
37	65	72.2	434	6	ABU03943 Human exp
38	65	72.2	434	6	ABU03934 Human exp
39	65	72.2	434	6	ABU03935 Human exp
40	65	72.2	434	6	ABU03935 Human exp
41	65	72.2	434	6	ABU03932 Human exp
42	65	72.2	434	6	ABU03930 Human exp
43	65	72.2	434	6	ABU03931 Human exp
44	65	72.2	434	6	ABU03937 Human exp
45	65	72.2	434	6	ABU03933 Human exp
46	65	72.2	434	6	ABU04797 Human alp
47	65	72.2	434	6	ABD85166 Rat enola
48	65	72.2	434	7	ADCS2079 Human adi
49	65	72.2	434	7	ADCS2079 Human adi
50	65	72.2	434	7	ADCS38355 Human pro
51	65	72.2	434	7	ADCS38355 Human pro
52	65	72.2	434	7	ADN95644 Human BEC
53	65	72.2	434	7	ADPE5133 Human eno
54	65	72.2	434	7	ADN04765 Antipsoxi
55	65	72.2	434	8	ADP12542 Protein e
56	65	72.2	434	8	ADP12542 Protein e
57	65	72.2	434	8	ADQ19151 Human pro
58	65	72.2	434	8	ADQ18898 Human sof
59	65	72.2	434	8	ADQ19129 Human sof
60	65	72.2	434	8	ADQ6748 Human eno
61	65	72.2	434	8	ADQ6750 Human eno
62	65	72.2	434	8	ADQ6746 Human eno
63	65	72.2	434	8	ABW80012 Tumour-as
64	65	72.2	434	8	ADP54139 Tumour-as
65	65	72.2	434	8	ADP54197 Human PRO
66	65	72.2	434	8	ADP23174 PRO polyP
67	65	72.2	434	9	ADW07263 Human hep
68	65	72.2	434	9	ADY75135 PRO polyP
69	65	72.2	434	9	ADY75135 Brain tum
70	65	72.2	434	9	ADZ70552 Human pro
71	65	72.2	434	9	ABE16877 Rat neuro
72	65	72.2	434	9	ABE16883 Human neu
73	65	72.2	434	9	ABE16875 Rat neuro
74	65	72.2	434	9	ABE16884 Rat neuro
75	65	72.2	434	5	ABE16885 Human neu
76	61	67.8	16	2	AAV43200 Schizophr
77	59	65.6	432	7	ADD26937 Human adi
78	59	65.6	434	9	AEA51198 Chicken g
79	59	65.6	434	9	ABE16886 Chicken n
80	58	64.4	15	2	AAV43203 Schizophr
81	56	62.2	396	9	ADY71461 Trichine
82	56	62.2	434	8	ADN22854 Bacteri
83	56	62.2	437	9	ADY71463 Trichine
84	55	61.1	433	4	ABB67951 Drosophi
85	51	56.7	66	5	ABP34165 Human hyd
86	51	56.7	68	3	AAE20166 Arabidops
87	51	56.7	77	3	AAE20165 Arabidops
88	51	56.7	78	3	AAE20164 Arabidops
89	51	56.7	211	8	ADX7369 Plant ful
90	51	56.7	245	8	ADX7369 Plant ful
91	51	56.7	313	7	ABW89093 Rice abio
92	51	56.7	340	7	ADM67652 D. salina
93	51	56.7	352	3	AAE37553 Arabidops
94	51	56.7	443	3	AAE37552 Arabidops
95	51	56.7	444	3	AAE37552 Arabidops
96	51	56.7	444	3	AAE60820 Arabidops
97	51	56.7	469	3	AAE37551 Arabidops

98	50	55.6	152	8	ADX80391	Adx80391 Plant full
99	50	55.6	226	8	ADX93896	Adx93896 Plant full
100	50	55.6	284	8	ADX74478	Adx74478 Plant full

## ALIGNMENTS

## RESULT 1

AAV43191  
ID AAV43191 standard; peptide; 16 AA.

AC AAV43191;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #1.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;

XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 2; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the

CC peptide to a platelet-containing fraction of blood, or a fraction

CC containing platelet-associated antibodies (PAA) shed from the platelets,

CC or preferably whole blood. The new peptides are able to differentiate

CC between plasma samples from schizophrenic and non-schizophrenic patients,

CC and can do so without having to first isolate the platelet-associated

CC antibodies (PAA) fraction

CC

CC

CC

CC

CC

CC

CC

KW platelet-associated antibody; diagnosis.

XX Synthetic.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 4; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the

CC peptide to a platelet-containing fraction of blood, or a fraction

CC containing platelet-associated antibodies (PAA) shed from the platelets,

CC or preferably whole blood. The new peptides are able to differentiate

CC between plasma samples from schizophrenic and non-schizophrenic patients,

CC and can do so without having to first isolate the platelet-associated

CC antibodies (PAA) fraction

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

## RESULT 2

AAV43204

ID AAV43204 standard; peptide; 16 AA.

AC AAV43204;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;

XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 2; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the

CC peptide to a platelet-containing fraction of blood, or a fraction

CC containing platelet-associated antibodies (PAA) shed from the platelets,

CC or preferably whole blood. The new peptides are able to differentiate

CC between plasma samples from schizophrenic and non-schizophrenic patients,

CC and can do so without having to first isolate the platelet-associated

CC antibodies (PAA) fraction

CC

CC

CC

CC

CC

CC

CC

XX Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the

CC peptide to a platelet-containing fraction of blood, or a fraction

CC containing platelet-associated antibodies (PAA) shed from the platelets,

CC or preferably whole blood. The new peptides are able to differentiate

CC between plasma samples from schizophrenic and non-schizophrenic patients,

CC and can do so without having to first isolate the platelet-associated

CC antibodies (PAA) fraction

XX

SQ Sequence 17 AA;

Query Match 86.7%; Score 78; DB 2; Length 17;

Best Local Similarity 93.8%; Pred. No. 0.00094;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAK 16

DB 1 LVVGLCTPQIKTGPAK 16

RESULT 4

AAV43197

ID AAV43197 standard; peptide; 17 AA.

XX AAV43197;

AC 11-JAN-2000 (first entry)

XX

DT Schizophrenic derived antibody binding epitope #7.

XX

DE Schizophrenic derived antibody; binding epitope; schizophrenia;

KM platelet-associated antibody; diagnosis.

XX

OS Synthetic.

XX

PN WO951725-A2.

XX

PD 14-OCT-1999.

XX

PF 30-MAR-1999; 99WO-IL000190.

XX

PR 02-APR-1998; 98IL-00123925.

XX

PA (YEDA ) YEDA RES & DEV CO LTD.

XX

PI Shintzky M, Deckmann M;

XX

DR WPI, 1999-611037/52.

XX

PT New peptides useful for diagnosis of schizophrenia.

XX

PS Claim 3; Page 21; 37pp; English.

XX

XX This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the

CC peptide to a platelet-containing fraction of blood, or a fraction

CC containing platelet-associated antibodies (PAA) shed from the platelets,

CC or preferably whole blood. The new peptides are able to differentiate

CC between plasma samples from schizophrenic and non-schizophrenic patients,

CC and can do so without having to first isolate the platelet-associated

CC antibodies (PAA) fraction

XX

SQ Sequence 17 AA;

Query Match 86.7%; Score 78; DB 2; Length 17;

Best Local Similarity 93.8%; Pred. No. 0.00094;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAK 16

DB 1 LVVGLCTPQIKTGPAK 16

RESULT 5

AAAG79784

ID AAAG79784 standard; protein; 458 AA.

XX AAAG79784;

AC 16-APR-2003 (first entry)

XX

DT Carbohydrate-associated protein (CHOP) -6.

XX

DE

XX Human; carbohydrate associated polypeptides; CHOP; cancer;

KM carbohydrate metabolism; diabetes; anaemia; hypoglycaemia; obesity;

KM glycogen storage disease; neurological dysfunction; gene therapy;

KM cell proliferation; actinic keratosis; arteriosclerosis; inflammation;

KM atherosclerosis; cirrhosis; hepatitis; psoriasis; autoimmune disorder;

KM acquired immunodeficiency syndrome; AIDS; humanized; transgenic;

KM Addison's disease; allergy; asthma; contact dermatitis; bronchitis; gout;

KM Hashimoto's thyroiditis; infection; reproduction; endometriosis;

KM polycystic ovary syndrome; ovarian hyperstimulation syndrome;

KM Down syndrome; cystic fibrosis; sickle cell anaemia; thalassemia;

KM myocarditis; cardiomyopathy; Alzheimer's disease; Parkinson's disease;

KM dementia; depression; epilepsy; Tourette's disorder; schizophrenia;

KM central nervous system; cerebral palsy; mood; anxiety; knockin.

XX

OS Homo sapiens.

XX

FT Key

FT location/Qualifiers

FT 1..455

FT /label= Enolase

FT /note= "Identified by BLAST\_DOMO"

FT 1..293

FT /label= Enolase lyase

FT /note= "Identified by BLAST\_PRODOM"

FT 2..456

FT /label= Enolase

FT /note= "Identified by HMWER\_PFAW"

FT 2..456

FT /label= Enolase

FT /note= "Identified by BLAST\_DOMO"

FT 7..456

FT /label= Enolase

FT /note= "Identified by BLAST\_DOMO"

FT 35..57

FT /label= Enolase protein

FT /note= "Identified by BLIMPS\_BLOCKS"

FT 38..52

FT /label= Enolase signature

FT /note= "Identified by BLIMPS\_PRINTS"

FT 113..129

FT /label= Enolase signature

FT /note= "Identified by BLIMPS\_PRINTS"

FT 153..202

FT /label= Enolase protein

FT /note= "Identified by BLIMPS\_BLOCKS"

FT 173..186

FT /label= Enolase signature

FT /note= "Identified by BLIMPS\_PRINTS"

FT 229..271

FT /label= Enolase protein

FT /note= "Identified by BLIMPS\_BLOCKS"

FT 275..440

FT /label= Lyase magnesium enolase

FT /note= "Identified by BLAST\_PRODOM"

FT 302..316

FT /label= Enolase protein

FT /note= "Identified by BLIMPS\_BLOCKS"

FT 314..362

FT /label= Enolase signature

FT	Protein	/note="Identified by PROFILESCAN"
FT		331..366
FT		/label=Enolase protein
FT		/note="Identified by BLIMPS_BLOCKS"
FT	Peptide	335..346
FT		/label=Enolase signature
FT	Peptide	/note="Identified by BLIMPS_PRINTS"
FT		351..375
FT		/label=Enolase signature
FT	Peptide	/note="Identified by BLIMPS_PRINTS"
FT		392..409
FT		/label=Enolase signature
FT	Protein	/note="Identified by BLIMPS_PRINTS"
FT		403..441
FT		/label=Enolase protein
FT		/note="Identified by BLIMPS_BLOCKS"
FT	Peptide	408..456
FT		/label=Enolase lyase glycolysis
FT		/note="Identified by BLAST_PRODOM"
XX	WM020297060-A2.	
XX		
XX	05-DEC-2002.	
XX		
XX	22-MAY-2002; 2002MO-US018354.	
XX		
PR	25-MAY-2001; 2001US-0293766P.	
PR	01-AUG-2001; 2001US-0309548P.	
PR	23-AUG-2001; 2001US-0314400P.	
PR	19-OCT-2001; 2001US-0343706P.	
PR	07-DEC-2001; 2001US-0337999P.	
PA	(INCYTE) INCYTE GENOMICS INC.	
PI	Swarnakar A, Gorvad AE, Hafalia AJA, Duggan BM, Emerling BM,	
PI	Ison CH, Nguyen DB, Lee EA, Yue H, Forsythe JV, Li JX,	
PI	Thangavelu K, Wallia NK, Burford N, Mason PM, Lal PG, Lee S,	
PI	Becha SD, Tang YT;	
DR	WPI; 2003-140462/13.	
XX	N-PSDB; ABA00836.	
XX		
PT	Novel human carbohydrate associated polypeptide, useful in diagnosis,	
PT	treatment and prevention of carbohydrate metabolism, cell proliferative,	
PT	autoimmune/inflammatory, reproductive, and neurological disorders.	
XX		
PS	Claim 1; Page 129-30; 141pp; English.	
XX		
CC	The sequences given in AAG979779-88 represent human carbohydrate	
CC	associated polypeptides (CHOP). The CHOP polypeptides and the nucleotide	
CC	sequences encoding them, are useful for diagnosing, treating and	
CC	preventing cancer, carbohydrate metabolic disorders (e.g. diabetes,	
CC	anaemia, hypoglycaemia, obesity, glycogen storage disease, neurological	
CC	dysfunctions), cell proliferative disorders (e.g. actinic keratosis,	
CC	autoimmunosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis),	
CC	autoimmune/inflammatory disorders (such as acquired immunodeficiency	
CC	syndrome (AIDS), Addison's disease, allergies, asthma, contact	
CC	dermatitis, bronchitis, gout, Hashimoto's thyroiditis), viral, bacterial,	
CC	fungal, parasitic, protozoal and helminthic infections, reproductive	
CC	disorders (e.g. endometriosis, polycystic ovary syndrome, ovarian	
CC	hyperstimulation syndrome), genetic disorders (e.g. Down syndrome, cystic	
CC	fibrosis, sickle cell anaemia, thalassemia), cardiac disorders (e.g.	
CC	myocarditis, cardiomyopathy), neurological disorders (e.g. Alzheimer's	
CC	disease, Parkinson's disease, dementia, depression, epilepsy, Tourette's	
CC	disorder, schizophrenia), and developmental disorders of central nervous	
CC	system (e.g. cerebral palsy), mental disorders (e.g. mood, anxiety). CHOP	
CC	proteins are useful in a number of drug screening techniques, and to	
CC	analyse the proteome of a tissue or cell type. CHOP cDNA is useful for	
CC	creating "knockin" humanized animals or transgenic animals to model human	
CC	diseases, in somatic or germline gene therapy, to generate a transcript	
CC	image of a tissue or cell type, for detecting differences in the	
CC	chromosomal location due to translocation, inversion, etc., among normal,	
CC	carrier or affected individuals, and as hybridization probes for mapping	

CC naturally occurring genomic sequences  
XX Sequence 458 AA;  
  
Query Match 82.2%; Score 74; DB 6; Length 458;  
Best Local Similarity 87.5%; Pred. No. 0.056;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Dy 1 LVVGLCTQIKTGPAK 16  
||| ||| ||| ||| |||  
Dd 407 LVVGLCTGQIKTGPYC 422

RESULT 6  
ADQ30526  
ID ADQ30526 standard; protein; 458 AA.  
XX  
AC ADQ30526;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Pancreas cancer marker - alpha enolase.  
XX  
KW Cytosolic; diagnosis; pancreatic cancer; antibody; antisense construct;  
XX differential expression.  
XX  
OS Homo sapiens.  
XX  
PN W02004055519-A2.  
XX  
PD 01-JUL-2004.  
XX  
PF 11-DEC-2003; 2003WC-EP014057.  
XX  
PR 17-DEC-2002; 2002EP-00028058.  
PR 05-NOV-2003; 2003EP-00025237.  
XX  
PA (HOF) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
XX  
PI Chen J, Hu L, Liu TH, Lu ZH, Shen Y;  
XX  
DR WPI; 2004-468121/46.  
XX  
PT New specific markers comprises at least one polypeptide up-regulated in  
PT pancreatic cancer, useful for diagnosing pancreatic cancer.  
PS Claim 1; SEQ ID NO 13; 381pp; English.

The invention relates to a marker (I) for diagnosis of pancreatic cancer comprising at least one polypeptide selected from 55 proteins up-regulated in pancreatic cancer (Table 2 and Table 3, given in the specification) or from 68 proteins with higher levels in pancreatic cancer compared to normal tissue (Table 6, given in the specification). (I) is a polypeptide for use as a marker or as a component of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. A compound (antibody, an antibody-derivative, an antibody fragment, a peptide, or an antisense construct) identified by screening methods using (I) is useful for treatment or prevention of pancreatic cancer. It is also useful for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. The current polypeptides were found to be differentially expressed in pancreatic tissue obtained from individuals suffering from pancreatic cancer as compared to healthy pancreatic tissue. They have been identified as suitable as markers of pancreatic cancer for early diagnosis of the disease. This sequence corresponds to a protein marker of the invention.

Sequence 458 AA;

Query Match 82.2%; Score 74; DB 8; Length 458;  
Best Local Similarity 87.5%; Pred. No. 0.056;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 DB 407 LVVGLCTGQIKTGPTC 422

RESULT 7  
 ADM08691  
 ID ADM08691 standard; protein; 458 AA.  
 AC ADM08691;  
 DT 24-MAR-2005 (first entry)

DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 28.  
 XX  
 KW gene targeting; hepatitis C virus infection; protein deactivation;  
 KM protein activation.

OS Homo sapiens.

PN EP1493750-A2.

PD 05-JAN-2005.

PF 28-JUN-2004; 2004EP-00015098.

PR 30-JUN-2003; 2003GB-00015248.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Berndt P, Kilby PM, Rugman P;

DR WPI; 2005-050476/06.

PT New targets for an antiviral compound having at least one down- and up-  
 PT regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
 PT outcomes, treating or preventing HCV infections.

PS Claim 1; SEQ ID NO 28; 346pp; English.

CC The invention comprises the amino acid sequences of protein targets for  
 CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
 CC invention are either up-regulated or down-regulated in HCV-infected  
 CC tissue. The proteins of the invention are useful in the preparation of a  
 CC medicament for the treatment or prevention of HCV infection. The present  
 CC amino acid sequence represents a human protein of the invention which is  
 CC down-regulated in HCV-infected tissue.

XX Sequence 458 AA;

Query Match 82.2%; Score 74; DB 9; Length 458;  
 Best Local Similarity 87.5%; Pred. No. 0.056;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 DB 407 LVVGLCTGQIKTGPTC 422

RESULT 8  
 AAY43202  
 ID AAY43202 standard; peptide; 16 AA.

AC AAY43202;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #12.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KW platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide  
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match 72.2%; Score 65; DB 2; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 0.053;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 DB 1 LVVGLCTGQIKTGPAAC 16

RESULT 9  
 AAY43196  
 ID AAY43196 standard; peptide; 17 AA.

AC AAY43196;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #6.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KW platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 3; Page 21; 37pp; English.

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XX      This sequence is a peptide of the invention, which binds antibodies found
CC      in elevated levels in body fluids of schizophrenic patients. The peptide
CC      is useful in an assay for the diagnosis of schizophrenia, by binding the
CC      peptide to a platelet-containing fraction of blood, or a fraction
CC      containing platelet-associated antibodies (PAA) shed from the platelets,
CC      or preferably whole blood. The new peptides are able to differentiate
CC      between plasma samples from schizophrenic and non-schizophrenic patients,
CC      and can do so without having to first isolate the platelet-associated
CC      antibodies (PAA) fraction
XX
SQ      Sequence 17 AA;
XX
Query Match      72.2%; Score 65; DB 2; Length 17;
Best Local Similarity 81.2%; Pred. No. 0.056;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 LVVGLCTGQIKTGAPC 16
        |||||
        1 LVVGLCTGQIKTGAPC 16
DB
RESULT 10
AAV43195
ID      AAV43195 standard; peptide; 18 AA.
XX
XX      AAV43195;
XX
DT      11-JAN-2000 (first entry)
XX
DE      Schizophrenic derived antibody binding epitope #5.
XX
KM      Schizophrenic derived antibody; binding epitope; schizophrenia;
XX      platelet-associated antibody; diagnosis.
XX
OS      Synthetic.
XX
PN      WO9951725-A2.
XX
PD      14-OCT-1999.
XX
PF      30-MAR-1999; 99WO-IL000190.
XX
PR      02-APR-1998; 98IL-00123925.
XX
PA      (YEDA ) YEDA RES & DEV CO LTD.
XX
PI      Shinitzky M, Deckmann M;
XX
DR      WPI; 1999-611037/52.
XX
PT      New peptides useful for diagnosis of schizophrenia.
XX
PS      Claim 3; Page 21; 37pp; English.
XX
XX      This sequence is a peptide of the invention, which binds antibodies found
CC      in elevated levels in body fluids of schizophrenic patients. The peptide
CC      is useful in an assay for the diagnosis of schizophrenia, by binding the
CC      peptide to a platelet-containing fraction of blood, or a fraction
CC      containing platelet-associated antibodies (PAA) shed from the platelets,
CC      or preferably whole blood. The new peptides are able to differentiate
CC      between plasma samples from schizophrenic and non-schizophrenic patients,
CC      and can do so without having to first isolate the platelet-associated
CC      antibodies (PAA) fraction
XX
SQ      Sequence 18 AA;
XX
Query Match      72.2%; Score 65; DB 2; Length 18;
Best Local Similarity 81.2%; Pred. No. 0.059;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 LVVGLCTGQIKTGAPC 16
        |||||
        1 LVVGLCTGQIKTGAPC 16
DB
RESULT 11
AAV43194
ID      AAV43194 standard; peptide; 19 AA.
XX
XX      AAV43194;
XX
DT      11-JAN-2000 (first entry)
XX
DE      Schizophrenic derived antibody binding epitope #4.
XX
KM      Schizophrenic derived antibody; binding epitope; schizophrenia;
XX      platelet-associated antibody; diagnosis.
XX
OS      Synthetic.
XX
PN      WO9951725-A2.
XX
PD      14-OCT-1999.
XX
PF      30-MAR-1999; 99WO-IL000190.
XX
PR      02-APR-1998; 98IL-00123925.
XX
PA      (YEDA ) YEDA RES & DEV CO LTD.
XX
PI      Shinitzky M, Deckmann M;
XX
DR      WPI; 1999-611037/52.
XX
PT      New peptides useful for diagnosis of schizophrenia.
XX
PS      Claim 3; Page 21; 37pp; English.
XX
XX      This sequence is a peptide of the invention, which binds antibodies found
CC      in elevated levels in body fluids of schizophrenic patients. The peptide
CC      is useful in an assay for the diagnosis of schizophrenia, by binding the
CC      peptide to a platelet-containing fraction of blood, or a fraction
CC      containing platelet-associated antibodies (PAA) shed from the platelets,
CC      or preferably whole blood. The new peptides are able to differentiate
CC      between plasma samples from schizophrenic and non-schizophrenic patients,
CC      and can do so without having to first isolate the platelet-associated
CC      antibodies (PAA) fraction
XX
SQ      Sequence 19 AA;
XX
Query Match      72.2%; Score 65; DB 2; Length 19;
Best Local Similarity 81.2%; Pred. No. 0.062;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 LVVGLCTGQIKTGAPC 16
        |||||
        3 LVVGLCTGQIKTGAPC 18
DB
RESULT 12
AAV43193
ID      AAV43193 standard; peptide; 20 AA.
XX
XX      AAV43193;
XX
DT      11-JAN-2000 (first entry)
XX
DE      Schizophrenic derived antibody binding epitope #3.
XX
KM      Schizophrenic derived antibody; binding epitope; schizophrenia;
XX      platelet-associated antibody; diagnosis.
XX
OS      Synthetic.
XX
PN      WO9951725-A2.
```

XX 14-OCT-1999.  
 PD 30-MAR-1999; 99WO-1L000190.  
 XX PF 02-APR-1998; 98IL-00123925.  
 XX PR (YEDA ) YEDA RES & DEV CO LTD.  
 XX PA Shintzky M, Deckmann M;  
 XX PI WPI; 1999-611037/52.  
 DR WPI; 1999-611037/52.  
 XX PT New peptides useful for diagnosis of schizophrenia.  
 XX PS Claim 3; Page 21; 37pp; English.  
 CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide  
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction  
 CC SQ Sequence 20 AA:

Query Match 72.2%; Score 65; DB 2; Length 20;  
 Best Local Similarity 81.2%; Pred. No. 0.064;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 4 LVVGLCTGQIKTGAPC 19

RESULT 13  
 ID AAY43192 standard; peptide; 28 AA.  
 XX AAY43192;  
 AC AAY43192;  
 XX 11-JAN-2000 (first entry)  
 DT 11-JAN-2000 (first entry)  
 XX Schizophrenic derived antibody binding epitope #2.  
 DE Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KW platelet-associated antibody; diagnosis.  
 XX Synthetic.  
 OS Synthetic.  
 XX MO9951725-A2.  
 XX 14-OCT-1999.  
 PD 14-OCT-1999.  
 XX 30-MAR-1999; 99WO-1L000190.  
 XX PF 02-APR-1998; 98IL-00123925.  
 XX PR (YEDA ) YEDA RES & DEV CO LTD.  
 XX PA Shintzky M, Deckmann M;  
 XX PI Shintzky M, Deckmann M;  
 XX WPI; 1999-611037/52.  
 DR WPI; 1999-611037/52.  
 XX New peptides useful for diagnosis of schizophrenia.  
 XX PT Claim 3; Page 21; 37pp; English.  
 PS Claim 3; Page 21; 37pp; English.  
 CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction  
 CC SQ Sequence 28 AA:

Query Match 72.2%; Score 65; DB 2; Length 28;  
 Best Local Similarity 81.2%; Pred. No. 0.086;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 12 LVVGLCTGQIKTGAPC 27

RESULT 14  
 ID ADU78952 standard; protein; 50 AA.  
 XX ADU78952;  
 AC ADU78952;  
 XX 27-JAN-2005 (first entry)  
 DT 27-JAN-2005 (first entry)  
 XX Human protein fragment, SEQ ID 325.  
 DE Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;  
 XX Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;  
 KW Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;  
 KW Alzheimer's disease; neurological disorder; phosphatase; enzyme.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX US2004226056-A1.  
 XX 11-NOV-2004.  
 PD 11-NOV-2004.  
 XX 09-FEB-2004; 2004US-00776013.  
 XX 22-DEC-1998; 98US-0113534P.  
 PR 12-MAR-1999; 99US-0124120P.  
 PR 30-JUN-1999; 99US-0141243P.  
 PR 21-DEC-1999; 99US-0046613P.  
 PR 17-OCT-2000; 2000US-0240790P.  
 PR 13-JUL-2001; 2001US-0304775P.  
 PR 10-SEP-2001; 2001US-00948904.  
 PR 12-OCT-2001; 2001US-00975072.  
 PR 15-JUL-2002; 2002US-00194967.  
 XX (MYRIAD GENETICS INC.  
 XX MYRIAD GENETICS INC.  
 XX ROCH J, BARTEL P, HEICHMAN K;  
 XX WPI; 2004-794772/78.  
 DR WPI; 2004-794772/78.  
 XX Selecting agents useful for treating Alzheimer's disease comprises  
 PT contacting focal adhesion kinase 2 with a test agent and measuring a  
 PT biological activity related to focal adhesion kinase 2 function with or  
 PT without the test agent.  
 XX Disclosure; SEQ ID NO 325; 247pp; English.  
 XX The present invention relates to a method for selecting agents that are  
 XX potentially useful for the treatment of Alzheimer's disease. The method  
 XX comprises contacting Focal Adhesion Kinase 2 (FAK2) with a test agent and  
 XX measuring a biological activity related to FAK2 function in the presence  
 XX and absence of the test agent. The method is useful for screening  
 XX compounds or agents that can be used to treat neurological disorders,  
 XX ailments and diseases including mild cognitive impairment, depression,  
 XX schizophrenia, obsessive-compulsive disorder, bipolar disorder, and

CC neurodegenerative diseases and disorders and motor neuron diseases and  
CC disorders such as Alzheimer's disease, Parkinson's disease, dementia with  
CC Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease,  
CC Alpers' disease, Leigh's disease, Pelizaeus-Merzbacher disease,  
CC Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett  
CC syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as  
CC for treating or preventing other diseases such as distalpendia, diabetes,  
CC obesity, cardiovascular diseases such as atherosclerosis and coronary  
CC heart disease. Also disclosed is the coding sequence for a novel human  
CC phosphatase called PN7740 (ADU78628 and ADU78629). PN7740 contains a  
CC protein phosphatase 2C domain, which likely acts to dephosphorylate  
CC specific phospho-serine or phospho-threonine residues on particular  
CC protein substrates. Although the precise role played by protein  
CC phosphatase 2Cs in Alzheimer's disease pathogenesis has yet to be  
CC defined, the inventors have discovered that fragments of PN7740 interact  
CC with the first phosphotyrosine binding domain (PTB) domain of Fe65 (also  
CC known as ABB1(710) or amyloid beta (A4) precursor protein-binding,  
CC family B, member 1, isoform B9 (710)), suggesting that PN7740 may well be  
CC involved, somehow. Fe65 is known to interact with the cytosolic C-terminal  
CC region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is  
CC critical to the pathogenesis of Alzheimer's disease, because it leads to  
CC the release of either toxic Abeta or trophic secreted APP (sAPP)  
CC metabolites. The present sequence is a potentially useful agent for  
CC Alzheimer's disease.

XX Sequence 50 AA;

Query Match 72.2%; Score 65; DB 8; Length 50;  
Best Local Similarity 81.2%; Pred. No. 0.14;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
|||||  
Db 24 LVVGLCTGQIKTGAPC 39

RESULT 15

ADT51055  
ID ADT51055 standard; protein; 156 AA.

XX ADT51055;

DT 13-JAN-2005 (first entry)

DE Cancer related protein sequence #218.

KM cytosstatic; gene therapy; vaccine; diagnosis; breast; colon; lung;  
KM ovarian; prostate; cancer.

OS Homo sapiens.

PN WC0004092338-A2.

PD 28-OCT-2004.

PF 12-APR-2004; 2004WO-US011104.

PR 11-APR-2003; 2003US-0462399P.

PT 01-JUL-2003; 2003US-0484333P.

PA (DIAD-) DIADEXUS INC.

PI Macina RA, Turner LR, Sun Y, Tam A;

DR WPI; 2004-766851/75.

PT New cancer specific nucleic acid (CasNA) molecules, useful for  
PT diagnosing, monitoring the presence of, or treating a patient with  
PT breast, colon, lung, ovarian, or prostate cancer.

PS Claim 12; SEQ ID NO 359; 891pp; English.

CC The invention relates to an isolated nucleic acid molecule (I)

CC selectively hybridizing to, or comprising at least 95% sequence identity  
CC to, any of the 362 nucleotide sequences fully defined in the  
CC specification. The nucleic acid molecules and polypeptides are useful for  
CC diagnosing, monitoring the presence of, or treating a patient with  
CC breast, colon, lung, ovarian, or prostate cancer. This sequence  
CC corresponds to a protein of the invention.

XX Sequence 156 AA;

Query Match 72.2%; Score 65; DB 8; Length 156;  
Best Local Similarity 81.2%; Pred. No. 0.38;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
|||||  
Db 106 LVVGLCTGQIKTGAPC 121

RESULT 16

ABU04377  
ID ABU04377 standard; protein; 269 AA.

XX ABU04377;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1043.

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KM protease; protease inhibitor; transporter; cytoskeletal protein;  
KM receptor; transcription factor; cancer; MHC;  
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCOS INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

PS Example 2; SEQ ID NO 1043; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for creating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,



CC Lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 6; Length 269;  
Best Local Similarity 81.2%; Pred. No. 0.6;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 219 LVVGLCTGQIKTGAPC 234

RESULT 17  
AD270357  
ID AD270357 standard; protein; 269 AA.

AC AD270357;  
DT 30-JUN-2005 (first entry)

XX Human protein from lung cancer marker gene ENOL, SEQ ID 42.

XX Tumor marker; lung tumor; cytostatic; neoplasm; expression;  
XX DNA microarray.

XX Homo sapiens.

PN WO2005032495-A2.

PD 14-APR-2005.

PF 01-OCT-2004; 2004WO-US034163.

PR 03-OCT-2003; 2003US-0508355P.

PA (FARB ) BAYER PHARM CORP.

PI Taylor I, Pauloski NR, Bigwood D;

XX WPI; 2005-285325/29.

DR N-PSDB; AD270356.

PT Providing a patient diagnosis for lung cancer comprises comparing the  
PT level of expression of genes or gene products in a biological sample from  
PT the patient with that from a normal individual.

XX Claim 3; SEQ ID NO 42; 60pp; English.

CC The invention relates to providing a patient diagnosis for lung cancer  
CC comprising comparing the level of expression of genes or gene products in  
CC a biological sample from the patient with the level of expression of  
CC genes or gene products in a biological sample from a normal individual.  
CC Also included are distinguishing between normal and disease tissues,  
CC monitoring the response of a patient being treated for lung cancer by  
CC administering an anti-cancer agent, identifying a compound useful for the  
CC treatment of lung cancer and an array for distinguishing between normal  
CC and disease tissues (comprising 2 or more probes corresponding to 2 or  
CC more genes selected from any of the 200 nucleotide sequences given in the  
CC specification, or 2 or more polypeptides comprising any of the 200 amino  
CC acid sequences given in the specification). In providing a patient  
CC diagnosis for lung cancer, one or more genes are selected from any of the  
CC 200 nucleotide sequences as mentioned in the specification, or one or  
CC more gene products are polypeptides selected from any of the 20 amino  
CC acid sequences mentioned in the specification. The methods are useful for  
CC detecting and treating lung cancer. These may also be used for designing,  
CC identifying and optimizing therapeutics for cancer. The present sequence  
CC represents a protein from one of the 200 lung cancer marker genes. Note:

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 9; Length 269;  
Best Local Similarity 81.2%; Pred. No. 0.6;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 219 LVVGLCTGQIKTGAPC 234

RESULT 18  
ABU04378  
ID ABU04378 standard; protein; 272 AA.

AC ABU04378;

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1044.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
XX proteinase; proteinase inhibitor; transporter; cytoskeletal protein;  
XX receptor; transcription factor; cancer; MHC;  
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

PA Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX Example 2; SEQ ID NO 1044; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.61;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 222 LVVGLCTGQIKTGAPC 237

RESULT 19  
ABU04375  
ID ABU04375 standard; protein; 272 AA.  
XX  
AC ABU04375;

DT 29-JAN-2003 (first entry)  
XX

DE Human expressed protein tag (EPT) #1041.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KM receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

PI WPI; 2003-040607/03.

DR

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

PS Example 2; SEQ ID NO 1041; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.61;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 222 LVVGLCTGQIKTGAPC 237

RESULT 20  
ABU04376  
ID ABU04376 standard; protein; 336 AA.  
XX  
AC ABU04376;

DT 29-JAN-2003 (first entry)  
XX

DE Human expressed protein tag (EPT) #1042.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KM receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

PI WPI; 2003-040607/03.

DR

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

PS Example 2; SEQ ID NO 1042; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SO Sequence 336 AA;

Query Match 72.2%; Score 65; DB 6; Length 336;  
Best Local Similarity 81.2%; Pred. No. 0.73;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 286 LVVGLCTGQIKTGAPC 301

RESULT 21

AAE38225 standard; protein; 420 AA.

AC AAE38225;

DT 20-NOV-2003 (first entry)

DE Human enzyme (ENZM) protein #17.

KM Human; enzyme; ENZM; immune disorder; infection; myocardial infarction;  
KM gene therapy; anaemia; acquired immune deficiency syndrome; infection;  
KM reproductive disorder; cardiovascular; eye; cell proliferation; cancer;  
KM AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence;  
KM infertility; atherosclerosis; metabolic disorder.

OS Homo sapiens.

PN WO2003052075-A2.

PD 26-JUN-2003.

PF 12-DEC-2002; 2002WO-US040161.

PR 14-DEC-2001; 2001US-0340357P.

PR 20-DEC-2001; 2001US-0342962P.

PR 21-DEC-2001; 2001US-0343558P.

PR 22-JAN-2002; 2002US-0351107P.

XX (INCYTE GENOMICS INC.

PI Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe ID, Khare R;  
PI Tran UK, Kabie AE, Richardson TW, Emerling BW, Lindquist EA;  
PI Baughn MR, Hafalla AJA, Jin P, Swarnakar A, Li JX, Margulis JP;  
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;

DR WPI; 2003-533016/50.

DR N-PSDB; AAD57505.

PT New human enzyme (ENZM) polypeptide, useful for preparing a composition  
PT for treating a disease associated with decreased expression or  
PT overexpression of ENZM e.g. cancer.

PS Claim 1; Page 283; 264pp; English.

XX The invention relates to human enzyme (ENZM) polypeptides and their  
CC corresponding polynucleotides. ENZM sequences are useful for preparing a  
CC composition for diagnosing or treating a disease or condition associated  
CC with decreased expression or overexpression of functional ENZM. The  
CC disorders include immune disorders (anaemia, allergy or asthma),  
CC infectious disorders (viral, fungal, parasitic or protozoal infection),  
CC immune deficiencies (acquired immune deficiency syndrome; AIDS),  
CC metabolic disorders (Addison's disease, diabetes or goitre), reproductive  
CC disorders (infertility or impotence), cardiovascular disorders  
CC (atherosclerosis or myocardial infarction), eye disorders and cell  
CC proliferative disorders (cancer). ENZM DNA is useful in gene therapy. The  
CC present sequence is human ENZM protein

SO Sequence 420 AA;

Query Match 72.2%; Score 65; DB 6; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.88;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 370 LVVGLCTGQIKTGAPC 385

RESULT 22

AAAB42064 standard; protein; 429 AA.

AC AAAB42064;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656.

KM Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KM vulnery; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;  
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KM antiviral; antibacterial; antifungal; antineuritic; antithyroid;  
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KM cardiovascular disease; diabetes mellitus; hypochyroidism; SCID; AIDS;  
KM cholesterol ester storage; systemic lupus erythematosus; infection;  
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KM thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US008621.

PR 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX (CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2000-602362/57.

DR N-PSDB; AAC76273.

PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease.

PS Claim 11; Page 2810-2811; 5507pp; English.

XX AACT74446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective; osteopathic;  
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
CC cardiac; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;  
CC antiviral; antifungal; antineuritic; antithyroid; and antianaemic. The  
CC sequences can be used for determining the presence of or predisposition  
CC to, or preventing or treating pathological conditions associated with an  
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX

CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
 CC used to treat cancers, proliferative disorders, neurodegenerative  
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone  
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
 XX

SO Sequence 429 AA;

Query Match 72.2%; Score 65; DB 3; Length 429;  
 Best Local Similarity 81.2%; Pred. No. 0.9;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 DB 379 LVVGLCTGQIKTGAPC 394

RESULT 23  
 ABU03938  
 ID ABU03938 standard; protein; 429 AA.  
 AC ABU03938;  
 XX  
 XX 29-JAN-2003 (first entry)  
 DT  
 XX  
 DE Human expressed protein tag (EPT) #604.  
 XX  
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KM protease; protease inhibitor; transporter; cytoskeletal protein;  
 KM receptor; transcription factor; cancer; MHC;  
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCOG INC.  
 XX  
 PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX  
 DR WPI; 2003-040607/03.  
 XX  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 XX Example 2; SEQ ID NO 604; 134pp; English.  
 PS  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor.  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/publib/published\_pct\_sequences  
 XX

SO Sequence 429 AA;

Query Match 72.2%; Score 65; DB 6; Length 429;  
 Best Local Similarity 81.2%; Pred. No. 0.9;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 DB 379 LVVGLCTGQIKTGAPC 394

RESULT 24  
 AAM14001  
 ID AAM14001 standard; protein; 433 AA.  
 XX  
 AC AAM14001;  
 XX  
 XX 23-MAY-1997 (first entry)  
 DT  
 XX  
 DE Enolase protein.  
 XX  
 KM PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE;  
 KM enolase; radioisotope; antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP08308584-A.  
 XX  
 PD 26-NOV-1996.  
 XX  
 PF 19-MAY-1995; 95JP-00145542.  
 XX  
 PR 19-MAY-1995; 95JP-00145542.  
 XX  
 PA (EIKE) EIKEN KAGAKU KK.  
 XX  
 DR WPI; 1997-059703/06.  
 XX  
 PT Introducing tyrosine residues into a protein for radioisotopic labelling  
 PT - by substitution, addition and/or insertion to a DNA coding for the  
 PT protein, antigenicity of the protein is unchanged by labelling.  
 XX  
 PS Disclosure; Page 10-11; 13pp; Japanese.  
 XX  
 XX This sequence represents the wild type human enolase (NSE) protein. The  
 CC primers represented by AAT60282-T60285 were used to amplify tyrosine  
 CC introduced versions of this sequence. The introduced tyrosine residues  
 CC combine a radioisotope in such a way as to have no substantial effect on  
 CC the antigenicity of the protein. The peptides with the introduced  
 CC tyrosine residue are prepared by expressing a recombinant DNA sequence,  
 CC where the tyrosine residue has been introduced via an insertion or  
 CC substitution into the wild type sequence. The peptides can then be used  
 CC in radioimmunoassays, as the introduction of the label does not alter the  
 CC antigenicity of the protein  
 XX

SO Sequence 433 AA;

Query Match 72.2%; Score 65; DB 2; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.9;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 DB 379 LVVGLCTGQIKTGAPC 394

DB 383 LVVGLCTGQIKTGAPC 398

# RESULT 25

AAW54357  
ID AAW54357 standard; protein; 433 AA.

AC AAW54357;

DT 14-AUG-1998 (first entry)

DE Alpha Enolase.

KM Endometrium; hyperplasia; adenocarcinoma; proliferative phase;  
2D gel electrophoresis; detection.

OS Homo sapiens.

PN WO9810291-A1.

PD 12-MAR-1998.

PF 05-SEP-1997; 97WO-GB002394.

PR 06-SEP-1996; 96GB-00018600.

PR 08-APR-1997; 97GB-00007132.

PA (CLIN-) CENT CLINICAL & BASIC RES.

PI Bjørnsen I, Larsen P, Fey SJ;

DR WPI, 1998-207057/18.

PT Biochemical markers of human endometrium - useful for, e.g. diagnosis of  
hyperplasia and adenocarcinoma.

PS Disclosure; Page 21; 77pp; English.

CC Proteins AAW54349-W54364 are examples of proteins produced in the  
endometrium during the hyperplasia, adenocarcinoma or proliferative phase  
of the endometrium. The presence and quantities of these proteins can be  
detected using 2D gel electrophoresis comparison of cell lysates. The  
proteins can be used as biochemical markers to detect the phase of the  
endometrium and can be measured in body fluids, obviating the need for  
endometrial biopsies

CC Sequence 433 AA;

Query Match 72.2%; Score 65; DB 2; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.9;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

# RESULT 26

ABU03944  
ID ABU03944 standard; protein; 433 AA.

AC ABU03944;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #610.

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
protease; protease inhibitor; transporter; cytoskeletal protein;  
receptor; transcription factor; cancer; MHC;  
major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

PA (ZYCO-) ZYCO INC.

PI Chicz RM, Tomlinson AJ, Urban RG;

DR WPI, 2003-040607/03.

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
cytoskeletal proteins, receptors or transcription factors), useful for  
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
leukemia.

PS Example 2; SEQ ID NO 610; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
fragment of a kinase, phosphatase, protease, protease inhibitor,  
transporter, cytoskeletal protein, receptor or transcription factor. The  
polypeptide is useful as an immunogenic composition for eliciting in a  
mammal an immunogenic response directed against any of the purified  
polypeptide. The purified polypeptide, or the antibody that binds to this  
polypeptide, is useful for treating cancer. The polypeptide is also  
useful for identifying compounds that binds to a naturally processed  
class I or class II MHC-binding polypeptide. The polypeptides and  
polynucleotides are particularly useful for treating or preventing  
myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
lymphoma or leukemia. These are also useful for screening agents for  
treating the above mentioned diseases. This sequence represents an  
expressed protein tag (EPT) isolated from human tissue for translational  
profiling. Note: This sequence does not appear in the printed  
specification but was obtained in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

CC Sequence 433 AA;

Query Match 72.2%; Score 65; DB 6; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.9;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

# RESULT 27

ABU03942  
ID ABU03942 standard; protein; 433 AA.

AC ABU03942;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #608.

KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
protease; protease inhibitor; transporter; cytoskeletal protein;  
receptor; transcription factor; cancer; MHC;  
major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.  
 XX  
 PN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCOS INC.  
 XX  
 PI Chicx RM, Tomlinson AJ, Urban RG;  
 XX  
 DR WPI; 2003-040607/03.  
 XX  
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 PS Example 2; SEQ ID NO 608; 134pp; English.  
 XX  
 CC The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (Ept) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 433 AA;  
 Query Match 72.2%; Score 65; DB 6; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.9;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 383 LVVGLCTGQIKTGAPC 398  
 ID ADQ30574 standard; protein; 433 AA.  
 AC ADQ30574;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Pancreas cancer marker - human alpha enolase.  
 XX  
 KW Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;  
 KM differential expression.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004055519-A2.

XX  
 PD 01-JUL-2004.  
 XX  
 PF 11-DEC-2003; 2003WO-EP014057.  
 XX  
 PR 17-DEC-2002; 2002EP-00028058.  
 PR 05-NOV-2003; 2003EP-00025237.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG P.  
 PA (SINO-) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
 XX  
 PI Chen J, Hu L, Liu TH, Lu ZH, Shen Y;  
 XX  
 DR WPI; 2004-488121/46.  
 XX  
 PT New specific markers comprises at least one polypeptide up-regulated in  
 PT pancreatic cancer, useful for diagnosing pancreatic cancer.  
 XX  
 PS Claim 1; SEQ ID NO 61; 381pp; English.  
 XX  
 CC The invention relates to a marker (I) for diagnosis of pancreatic cancer  
 CC comprising at least one polypeptide selected from 55 proteins up-  
 CC regulated in pancreatic cancer (Table 2 and Table 3, given in the  
 CC specification) or from 68 proteins with higher levels in pancreatic  
 CC cancer compared to normal tissue (Table 6, given in the specification).  
 CC (1) is a polypeptide for use as a marker or as a component of a marker  
 CC for diagnosis of pancreatic cancer and/or the susceptibility to  
 CC pancreatic cancer. A compound (antibody, an antibody-derivative, an  
 CC screening method using (I) is useful for treatment or prevention of  
 CC pancreatic cancer. It is also useful for the preparation of a diagnostic  
 CC composition for diagnosing pancreatic cancer or a predisposition for  
 CC differentially expressed in pancreatic tissue obtained from individuals  
 CC suffering from pancreatic cancer as compared to healthy pancreatic  
 CC tissue. They have been identified as suitable as markers of pancreatic  
 CC cancer for early diagnosis of the disease. This sequence corresponds to a  
 CC protein marker of the invention.  
 XX  
 SQ Sequence 433 AA;  
 Query Match 72.2%; Score 65; DB 8; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.9;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 383 LVVGLCTGQIKTGAPC 398  
 ID ABB57379 standard; protein; 434 AA.  
 AC ABB57379;  
 XX  
 DT 07-AUG-2003 (revised)  
 DT 08-MAR-2002 (first entry)  
 XX  
 DE Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 10.  
 XX  
 KW Rat; heart; cardiast; myocardial necrosis; cardiac hypertrophy;  
 KM cardiac insufficiency.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN WO200183705-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 27-APR-2001; 2001WO-JP003700.  
 XX  
 PR 27-APR-2000; 2000JP-00126741.

XX (KYOW) KYOWA HAKKO KOGYO KK.  
 PA Yamada Y, Sekine S, Kikuchi Y, Sakurada K;  
 PI WPI; 2002-075160/10.  
 DR N-PSDB; ABI99919.  
 XX  
 PT Gene having differential expression in fetal and adult heart tissue  
 PT useful for screening potential drugs for promoting repair of damage  
 PT caused by myocardial necrosis.  
 PS  
 PS Claim 53; Page 98-100; 171pp; Japanese.  
 CC The invention relates to gene sequences (ABI99915-ABI99934) having  
 CC modified expression in fetal heart tissue as compared to adult heart  
 CC tissue and the encoded proteins (AB57375-AB57392). The genes have  
 CC cardiac activity and may be useful in the promotion of the repair of  
 CC damage to heart tissue caused by myocardial necrosis. The gene sequences  
 CC are useful for screening potential compounds for the ability to influence  
 CC disease associated with myocardial necrosis. Drugs identified by the  
 CC screening methods may be used to treat and prevent disease with which  
 CC myocardial necrosis is associated, such as cardiac hypertrophy and  
 CC cardiac insufficiency. Diagnosis of diseases such as those above is also  
 CC disclosed. (Updated on 07-AUG-2003 to correct OS field.)  
 CC  
 SO Sequence 434 AA;  
 SQ  
 Query Match 72.2%; Score 65; DB 5; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.91;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 384 LVVGLCTGQIKTGAPC 399  
 RESULT 30  
 ID ABP65147 standard; protein; 434 AA.  
 AC ABP65147;  
 XX  
 DT 12-NOV-2002 (first entry)  
 XX  
 DE Hypoxia-regulated protein #21.  
 XX  
 KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnerrary; gynecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;  
 KW inflammation; erythropoiesis; hair loss; human.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200246465-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 10-DEC-2001; 2001WO-GB005458.  
 XX  
 PR 08-DEC-2000; 2000GB-00030076.  
 PR 08-FEB-2001; 2001GB-0003156.  
 PR 25-OCT-2001; 2001GB-00025666.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner WN;  
 XX  
 DR WPI; 2002-627238/67.  
 XX

PT Identifying a gene involved in disease for treating hypoxia-regulated  
 PT conditions, comprises comparing the transcriptome/proteome of two cell  
 PT types under different conditions and identifying a differentially  
 PT regulated gene.  
 PS  
 PS Claim 35; Page 344; 538pp; English.  
 CC  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/proteome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV7873-ABV78116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating a disease in a  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC biological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
 CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss  
 CC  
 SO Sequence 434 AA;  
 SQ  
 Query Match 72.2%; Score 65; DB 5; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.91;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 384 LVVGLCTGQIKTGAPC 399

Search completed: April 3, 2006, 08:04:17  
 Job time : 85 secs

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OM protein - protein search, using SW model

Run on: Apr11 3, 2006, 08:03:01 ; Search time 15 Seconds  
(without alignments)  
102.631 Million cell updates/sec

Title: US-09-647-457F-3

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	2	I37360 phosphopyruvate hy
2	65	72.2	395	2	I50026 phosphopyruvate hy
3	65	72.2	433	2	A37210 phosphopyruvate hy
4	65	72.2	434	1	NOHUG phosphopyruvate hy
5	65	72.2	434	1	NOMSB phosphopyruvate hy
6	65	72.2	434	1	NOXL phosphopyruvate hy
7	65	72.2	434	2	JC1039 phosphopyruvate hy
8	65	72.2	434	2	JC4186 phosphopyruvate hy
9	65	72.2	434	2	JC4187 phosphopyruvate hy
10	65	72.2	434	2	S06756 phosphopyruvate hy
11	65	72.2	434	2	S10246 phosphopyruvate hy
12	65	72.2	434	2	S10247 phosphopyruvate hy
13	65	72.2	434	2	S02072 phosphopyruvate hy
14	65	72.2	434	2	A29170 phosphopyruvate hy
15	65	72.2	434	2	A32132 phosphopyruvate hy
16	65	72.2	434	2	A24742 phosphopyruvate hy
17	65	72.2	434	2	A23126 phosphopyruvate hy
18	56	62.2	434	2	T25040 phosphopyruvate hy
19	55	62.2	433	2	S07586 phosphopyruvate hy
20	55	61.1	433	2	A23850 phosphopyruvate hy
21	53	58.9	431	2	A53665 phosphopyruvate hy
22	52	57.8	446	2	T03267 probable phospho
23	51	56.7	326	2	JQ1186 phosphopyruvate hy
24	51	56.7	444	2	JQ1185 phosphopyruvate hy
25	51	56.7	444	2	JQ1187 phosphopyruvate hy
26	51	56.7	446	2	T02221 phosphopyruvate hy
27	50	55.6	445	2	S39203 phosphopyruvate hy
28	49	54.4	444	2	T12341 phosphopyruvate hy
29	49	54.4	446	2	S16257 phosphopyruvate hy

30	48	53.3	372	2	S24996 phosphopyruvate hy
31	47.5	52.8	1520	2	T27283 hypothetical prote
32	47.5	52.8	2346	2	T15840 phosphopyruvate hy
33	47	52.2	446	2	S42206 phosphopyruvate hy
34	46.5	51.7	437	1	NOBY phosphopyruvate hy
35	46.5	51.7	437	1	NOBY2 phosphopyruvate hy
36	46	51.1	125	1	VSMTA2 phosphopyruvate hy
37	46	51.1	137	2	S07648 phosphopyruvate hy
38	46	51.1	477	2	B96768 phosphopyruvate hy
39	45	50.0	329	2	AH3559 protein enolase p2
40	44	48.9	43	2	S13581 choriogadon [limpor
41	44	48.9	959	2	S48962 MSH1 protein - yea
42	43	47.8	85	2	E70531 hypothetical prote
43	43	47.8	456	2	S73562 phosphopyruvate hy
44	43	47.8	687	2	A49636 soluble yascular e
45	43	47.8	1006	2	T00050 hypothetical prote
46	43	47.8	1338	2	S09982 protein-tyrosine k
47	42	46.7	131	2	T32769 hypothetical prote
48	42	46.7	142	2	A71097 hypothetical prote
49	42	46.7	231	2	D64486 hypothetical prote
50	42	46.7	261	2	A53191 hypothetical prote
51	42	46.7	261	2	S33356 hypothetical prote
52	42	46.7	345	2	A05279 surface antigen 51
53	42	46.7	429	2	H83191 enolase PA3635 [im
54	42	46.7	497	2	AG3134 N-ethylammelane ch
55	42	46.7	498	2	E98153 hypothetical prote
56	41	45.6	131	2	T32880 hypothetical prote
57	41	45.6	137	2	S22515 thionin precursor,
58	41	45.6	177	2	A37408 betacellulin precu
59	41	45.6	178	2	JC1467 betacellulin precu
60	41	45.6	585	2	RR8087 protein B0454.6 [l
61	41	45.6	3175	1	RRWVEV genome polyprotein
62	40.5	45.0	335	2	T18906 hypothetical prote
63	40.5	45.0	1295	2	A32901 g1p1 protein precu
64	40.5	45.0	2531	2	S18188 notch protein homo
65	40.5	45.0	2531	2	A46019 notch-1 protein -
66	40.5	45.0	2555	2	A40043 notch protein homo
67	40.5	45.0	3106	1	S53868 laminin alpha-2 ch
68	40	44.4	132	2	T20463 hypothetical prote
69	40	44.4	277	2	C82571 hypothetical prote
70	40	44.4	314	2	H86532 hypothetical prote
71	40	44.4	314	2	F72090 probable chianin b
72	40	44.4	433	2	H70141 enolase (eno) homo
73	40	44.4	440	2	T32190 hypothetical prote
74	40	44.4	574	2	T34208 hypothetical prote
75	40	44.4	3672	2	T23433 probable laminin a
76	40	44.4	3704	2	T37316 hypothetical prote
77	39.5	43.9	372	2	T29359 hypothetical prote
78	39.5	43.9	440	2	S43113 phosphopyruvate hy
79	39.5	43.9	772	2	S33659 integrin beta 2 ch
80	39.5	43.9	2524	2	A35844 Korch protein - Af
81	39	43.3	139	2	T23371 hypothetical prote
82	39	43.3	220	2	T49564 hypothetical prote
83	39	43.3	293	2	T31184 hypothetical prote
84	39	43.3	314	2	T27686 hypothetical prote
85	39	43.3	364	2	G86180 hypothetical prote
86	39	43.3	374	2	T20110 hypothetical prote
87	39	43.3	513	2	A24309 genome polyprotein
88	39	43.3	522	1	GNWVR1 structural polyp
89	39	43.3	665	2	E88979 structural polyp
90	39	43.3	689	2	T52060 protein F3784.8 [l
91	39	43.3	992	1	GNWVR3 protein MEDA [limp
92	39	43.3	1063	1	GNWVR7 structural polyp
93	39	43.3	1063	1	GNWVR4 structural polyp
94	39	43.3	1063	1	GNWVR4 structural polyp
95	39	43.3	1239	1	VHWVEE structural polyp
96	39	43.3	1240	1	VHWVEE structural polyp
97	39	43.3	1241	2	S26373 genome polyprotein
98	39	43.3	1242	2	A56605 structural polyp
99	39	43.3	1242	2	S72350 structural polyp
100	39	43.3	2054	2	T46612 multi PDZ domain p

## ALIGNMENTS

RESULT 1  
137360 phosphopyruvate hydratase (EC 4.2.1.11), lung - human  
N/Alternate names: enolase  
C/Species: Homo sapiens (man)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: I37360; S22071  
R/Yerna, M.; Kurl, R.N.  
Biochem. Int. 30, 293-303, 1993  
A/Title: Human lung enolase: cloning and sequencing of cDNA and its inducibility with de  
A/Reference number: I37360  
A/Accession: I37360  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-458 <VER>  
A/Cross-references: UNIPROT:O05524; UNIPARC:UPI0000129F55; EMBL:X66610; NID:g31178; PIDN:  
A/Note: submitted to the EMBL Data Library, June 1992  
C/Function:  
A/Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
A/Pathway: gluconeogenesis; glycolysis  
C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
F/43/Binding site: magnesium 2 (Set) #status predicted  
F/219/Active site: Glu, Lys #status predicted  
F/254,308,336/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 82.2%; Score 74; DB 2; Length 458;  
Best Local Similarity 87.5%; Pred. No. 0.00059;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 407 LVVGLCTGQIKTGPTC 422

RESULT 2  
150026 phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)  
N/Alternate names: alpha-enolase  
C/Species: Alligator mississippiensis (American alligator)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: I50026  
R/Hedger, S.B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994  
A/Title: Molecular evidence for the origin of birds.  
A/Reference number: A53470; MUID:94195794; PMID:8146164  
A/Accession: I50026  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown; translate  
A/Molecule type: mRNA  
A/Residues: 1-395 <HED>  
A/Cross-references: UNIPROT:P42897; UNIPARC:UPI0000129F57; GB:U28078; NID:g472796; PIDN:  
A/Status: preliminary; translated from GB/EMBL/DBJ  
C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 395;  
Best Local Similarity 81.2%; Pred. No. 0.013;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 362 LVVGLCTGQIKTGAPC 377

RESULT 3  
A37210 phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit  
N/Alternate names: enolase beta  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 05-Oct-2004  
C/Accession: A37210

R/Chin, C.C.Q.  
U. Protein Chem. 9, 427-432, 1990  
A/Title: The primary structure of rabbit muscle enolase.  
A/Reference number: A37210; MUID:91113295; PMID:2275753  
A/Accession: A37210  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-433 <CHI>  
A/Cross-references: UNIPROT:P25704; UNIPARC:UPI000017606F  
C/Superfamily: enolase  
C/Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase  
F/1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 4  
NOHUG  
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human  
N/Alternate names: enolase gamma; neuron-specific enolase  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Oct-2004  
C/Accession: J00060; S16163; S02077; S56569; S02616; S38303  
R/Oliva, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.  
Gene 79, 355-360, 1999  
A/Title: Cloning, expression and sequence homologues of cDNA for human gamma enolase.  
A/Reference number: J00060; MUID:90006764; PMID:2792767  
A/Accession: J00060  
A/Molecule type: mRNA  
A/Residues: 1-434 <OLI>  
A/Cross-references: UNIPROT:P09104; UNIPARC:UPI000013CGF1; GB:M22349; NID:g951199; PIDN:  
R/Oliva, D.; Gali, L.; Feo, S.; Giallongo, A.  
Genomics 10, 157-165, 1991  
A/Title: Complete structure of the human gene encoding neuron-specific enolase.  
A/Reference number: S16163; MUID:91257823; PMID:2045099  
A/Accession: S16163  
A/Molecule type: DNA  
A/Residues: 1-434 <OLI>  
A/Cross-references: UNIPARC:UPI000013CGF1; GB:X51956; NID:g31164; PIDN:CAA36215.1; PID:  
R/McLeese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.  
Eur. J. Biochem. 178, 413-417, 1988  
A/Title: Complete amino acid sequence of the neuron-specific gamma isozyme of enolase  
A/Reference number: S02077; MUID:89091176; PMID:3208766  
A/Accession: S02077  
A/Molecule type: mRNA  
A/Residues: 2-3, 'Q', 'S', '239', 'W', '241-434' <MCA>  
A/Cross-references: UNIPARC:UPI000015B77; EMBL:X13120; NID:g31145; PIDN:CAA31512.1; PI:  
A/Note: part of this sequence was confirmed by protein sequencing  
A/Note: 264-Ala and 395-Ala were also found  
R/Van Obergerghen, E.; Kamholz, J.; Bishop, J.G.  
J. Neurosci. Res. 19, 450-456, 1988  
A/Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tum  
A/Reference number: S56569; MUID:88259288; PMID:3385803  
A/Accession: S56569  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 'GC', '29-126', 'N', '128-434' <VAN>  
A/Cross-references: UNIPARC:UPI000016A897; GB:M36768; NID:g182117; PIDN:AAA52388.1; PID:  
R/Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.  
FEBS Lett. 222, 139-143, 1987  
A/Title: Sequence conservation in the 3'-untranslated regions of neuron-specific enolase  
A/Reference number: S02616; MUID:88005129; PMID:3653393  
A/Accession: S02616  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 425-434 <DAY>  
A/Cross-references: UNIPARC:UPI0000172FAB; GB:Y00691; GB:M27610

R.Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.  
 Biochim. Biophys. Acta 1158, 120-128, 1993  
 A>Title: Characterization of an epitope specific to the neuron-specific isoform of human  
 A:beta/A4-protein.  
 A:Reference number: S38303; MUID:94002176; PMID:7691181  
 A:Accession: S38303  
 A:Molecule type: protein  
 A:Residues: 156-173 <HAR>  
 A:Cross-references: UNIPARC:UPI0000172FAPC  
 C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mamma  
 C:Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of neuro  
 C:Genetics:  
 A:Gene: GDB:EMO2  
 A:Cross-references: GDB:119872; OMIM:131360  
 A:Map position: 12p13-12p13  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2  
 C:Function:  
 C:Complex: homodimer  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;  
 F:2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>  
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQGIKTPAC 16  
 Db 384 LVVGLCTQGIKTPAC 399

RESULT 5  
 NOMSB  
 phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse  
 N:Alternate names: enolase beta  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text\_change 05-Oct-2004  
 C:Accession: S17109; S18036; S29675; A33921  
 R:Landmark, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.  
 Submitted to the EMBL Data Library, September 1991  
 A:Reference number: S17109  
 A:Accession: S17109  
 A:Molecule type: DNA  
 A:Residues: 1-434 <LAM>  
 A:Cross-references: UNIPROT:P21550; UNIPARC:UPI0000001937; EMBL:X61600; NID:G50848; PIDN  
 R:Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.  
 Submitted to the EMBL Data Library, October 1991  
 A:Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th  
 A:Reference number: S18036  
 A:Accession: S18036  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <PET>  
 A:Cross-references: UNIPARC:UPI0000001937; EMBL:X62667; NID:G50143; PIDN:CAA44540.1; PID  
 R:Lazar, M.; Landmark, N.; Brosset, S.; Lucas, M.; Keller, A.  
 Submitted to the EMBL Data Library, February 1991  
 A:Reference number: S29675  
 A:Accession: S29675  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <LAZ>  
 A:Cross-references: UNIPARC:UPI0000001937; EMBL:X57747; NID:G50846; PIDN:CAA40913.1; PID  
 R:Landmark, N.; Maza, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Gros, F.; Legault-Demar  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989  
 A>Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre  
 A:Reference number: A33921; MUID:89282789; PMID:2734297  
 A:Accession: A33921  
 A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 59-233; 'NA', 236-434 <LA2>  
 A:Cross-references: UNIPARC:UPI000016C036; GB:M20745; NID:G193029; PIDN:AAA37554.1; PI  
 A:Experimental source: skeletal muscle  
 C:Genetics:  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C:Function:  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to ph  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolys  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQGIKTPAC 16  
 Db 384 LVVGLCTQGIKTPAC 399

RESULT 6  
 NOXL  
 phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog  
 N:Alternate names: enolase ENO1  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text\_change 05-Oct-2004  
 C:Accession: S00463  
 R:Segall, N.; Shrutkowski, A.; Dworkin, M.B.; Dworkin-Raschl, E.  
 Biochem. J. 251, 31-39, 1988  
 A>Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterizatio  
 A:Reference number: S00463; MUID:88268812; PMID:3390159  
 A:Accession: S00463  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <SEG>  
 A:Cross-references: UNIPROT:P08734; UNIPARC:UPI0000171530; EMBL:Y00718; NID:G64679; PII  
 C:Genetics:  
 A:Gene: ENO1  
 C:Function:  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to ph  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magn  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQGIKTPAC 16  
 Db 384 LVVGLCTQGIKTPAC 399

RESULT 7  
 JCI1039  
 phosphopyruvate hydratase (EC 4.2.1.11) - rat  
 N:Alternate names: neuron-specific enolase  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Mar-1993 #sequence revision 19-Oct-1995 #text\_change 03-May-1996  
 C:Accession: JCI1039  
 R:Zhao, C.; Wang, L.B.; Song, X.W.; Zhang, J.Y.  
 Chinese Biochem. J. 10, 270-273, 1994  
 A>Title: cDNA cloning and sequencing of the NSF gene from rat brain.  
 A:Reference number: JCI1039  
 A:Accession: JCI1039  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <ZHA>

A:Cross-references: UNIPARC:UPI000017606E  
 A:Experimental source: brain, Miscar  
 C:Comment: This enzyme is a specific marker protein for the development of nervous system  
 C:Gene: nse  
 A:Gene: nse  
 C:Superfamily: enolase  
 C:Keywords: brain; carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTCQIKTGAPC 399

## RESULT 8

JC4186

phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken  
 N:Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase  
 C:Species: Gallus gallus (chicken)  
 C>Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: JC4186

R:Tanaka, M.; Maeda, K.; Nakashima, K.  
 J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphatase  
 A:Reference number: JC4186; PMID:95355305; PMID:7629021

A:Residues: 1-434 <TRAN>  
 A:Molecule type: mRNA

A:Cross-references: UNIPROT:P51913; UNIPARC:UPI0000171311; DDBJ:D37900; NID:G974175; PIR  
 C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which  
 rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein  
 F:44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTCQIKTGAPC 399

## RESULT 9

JC4187

phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken  
 N:Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase  
 C:Species: Gallus gallus (chicken)  
 C>Date: 14-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: JC4187

R:Tanaka, M.; Maeda, K.; Nakashima, K.  
 J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphatase  
 A:Reference number: JC4186; PMID:95355305; PMID:7629021

A:Accession: JC4187  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <TRAN>  
 A:Cross-references: UNIPROT:P07322; UNIPARC:UPI0000171312; DDBJ:D37901; NID:G974177; PIR  
 C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which  
 rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb  
 C:Superfamily: enolase  
 C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein  
 F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTCQIKTGAPC 399

## RESULT 10

S06756

phosphopyruvate hydratase (EC 4.2.1.11) beta - human  
 N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, m  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
 C:Accession: S06756; S14759; S15933; S33330; S08685; S31650

R:Peshevaria, M.; Hinks, L.J.; Day, I.N.M.  
 Nucleic Acids Res. 17, 8862, 1989

A:Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genom  
 A:Reference number: S06756; PMID:90067857; PMID:2587223

A:Accession: S06756  
 A:Molecule type: mRNA

A:Residues: 1-434 <PRS>  
 A:Cross-references: UNIPROT:P13929; UNIPARC:UPI000016A896; EMBL:X16504; NID:G31169; PIR  
 R:Peshevaria, M.; Day, I.N.M.  
 Biochem. J. 275, 427-433, 1991

A:Title: Molecular structure of the human muscle-specific enolase gene (ENOS).  
 A:Reference number: S14759; PMID:91222137; PMID:1840492

A:Accession: S14759  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA

A:Residues: 1-434 <PE2>  
 A:Cross-references: UNIPARC:UPI000016A896; EMBL:X55976  
 R:Call, L.; Feo, S.; Oliva, D.; Giallongo, A.  
 Nucleic Acids Res. 18, 1893, 1990

A:Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE)  
 A:Reference number: S15933; PMID:90245587; PMID:2336366

A:Accession: S15933  
 A:Molecule type: mRNA

A:Residues: 1-84, 'A', '86-161, 'K', '163-434 <CAL>  
 A:Cross-references: UNIPARC:UPI0000161C26; EMBL:X51957; NID:G34788; PIR:CAA36216.1; PIR  
 R:Giallongo, A.; Venturilla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.  
 Eur. J. Biochem. 214, 367-374, 1993

A:Title: Structural features of the human gene for muscle-specific enolase. Differential  
 A:Reference number: S33330; PMID:93292497; PMID:8513787

A:Accession: S33330  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA

A:Residues: 1-161, 'K', '163-434 <GIA>  
 A:Cross-references: UNIPARC:UPI000016A894; EMBL:X56832; NID:G31166; PIR:CAA40163.1; PIR

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990  
 C:Gene: ENOS3  
 A:Cross-references: GDB:119873; OMIM:131370

A:Map position: 17pter-17p12  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skel

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTCQIKTGAPC 399

## RESULT 11

S10246

phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse  
 N:Alternate names: 2-phosphoglycerate dehydratase; enolase alpha  
 C:Species: Mus musculus (house mouse)  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C:Accession: S10246; A56781

R:Kaghad, M.; Dumont, X.; Chaloin, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C  
 Nucleic Acids Res. 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
 A:Reference number: S10246; MUID:90301487; PMID:2362815  
 A:Accession: S10246  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <KAG>  
 A:Cross-references: UNIPROT:P17182; UNIPARC:UPI0000161F48; EMBL:X52379; NID:G55490; PIDN  
 R:Botallo, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.  
 A:Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch  
 olesterol.  
 A:Reference number: A56781; MUID:93152553; PMID:8427861  
 A:Accession: A56781  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-185, 'X',  
 A:Cross-references: UNIPARC:UPI0000176064; UNIPARC:UPI0000176065; UNIPARC:UPI0000176066;  
 A:Experimental source: peritoneal macrophages  
 A:Note: sequence modified after extraction from NCBI backbone  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 12  
 S10247  
 phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
 C:Accession: S10247  
 R:Kashad, M.; Dumont, X.; Chalton, P.; Lelias, J.M.; Lemande, N.; Lucas, M.; Lazar, M.; C  
 Nucleic Acids Res. 18, 3638, 1990  
 A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
 A:Reference number: S10246; MUID:90301487; PMID:2362815  
 A:Accession: S10247  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <KAG>  
 A:Cross-references: UNIPROT:P17183; UNIPARC:UPI0000001520; EMBL:X52380; NID:G55494; PIDN  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 13  
 S02072  
 phosphopyruvate hydratase (EC 4.2.1.11) beta - rat  
 N:Alternate names: enolase beta; enolase, muscle-specific  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
 C:Accession: S02072  
 R:Onahima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.  
 FEBS Lett. 242, 425-430, 1989  
 A:Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta  
 A:Reference number: S02072; MUID:89121113; PMID:2914621  
 A:Accession: S02072  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <OHS>  
 A:Cross-references: UNIPROT:P15429; UNIPARC:UPI0000167947; EMBL:X00979; NID:G57781; PIDN  
 A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-Asp

C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 14  
 A29170  
 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human  
 N:Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
 C:Accession: S11696; A29170; S52858; A39183  
 R:Giallongo, A.; Olive, D.; Cali, L.; Barba, G.; Barbieri, G.; Feo, S.  
 Eur. J. Biochem. 190, 567-573, 1990  
 A:Title: Structure of the human gene for alpha-enolase.  
 A:Reference number: S11696; MUID:90323004; PMID:2373081  
 A:Accession: S11696  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-434 <GTA>  
 A:Cross-references: UNIPROT:P06733; UNIPARC:UPI000013C9AF; EMBL:X16288; NID:G31172; PI  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989  
 R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986  
 A:Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpi  
 A:Reference number: A29170; MUID:86313654; PMID:3529090  
 A:Accession: A29170  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <G12>  
 A:Cross-references: UNIPARC:UPI000013C9AF; GB:M14328; NID:G182113; PIDN:AA52387.1; PI  
 A:Note: the authors translated the codon AAG for residue 193 as His  
 R:Walter, M.; Leidenberger, F.A.; Schwepppe, K.W.; Berg, H.; Northemann, W.  
 submitted to the EMBL Data Library, February 1995  
 A:Description: Autoreactive epitopes within the human alpha-enolase and their recogniti  
 A:Reference number: S52858  
 A:Accession: S52858  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-251, 'S', 253-434 <MAL>  
 A:Cross-references: UNIPARC:UPI000016A207; EMBL:X84907; NID:G693932; PIDN:CAA59331.1; F  
 R:Miles, L.A.; Dahlberg, C.M.; Plencia, J.; Felez, J.; Kato, K.; Plow, E.F.  
 Biochemistry 30, 1682-1691, 1991  
 A:Title: Role of cell-surface lysines in plasminogen binding to cells: identification c  
 A:Reference number: A39183; MUID:91129243; PMID:1847072  
 A:Accession: A39183  
 A:Molecule type: Protein  
 A:Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MT>  
 A:Cross-references: UNIPARC:UPI0000176068; UNIPARC:UPI0000176069  
 C:Genetics:  
 A:Gene: GDB:EN01  
 A:Cross-references: GDB:119871; OMIM:172430  
 A:Map position: 1p36-1p36  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C:Function:  
 A:Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosphogly  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
 F,2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAT>

Query Match 72.2%; Score 65; DB 2; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16  
 |||||  
 Db 384 LVVGLCTGQIKTGAPC 399

```
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 15
A23132
phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck
N:Alternate names: enolase alpha; tau-crystallin
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 05-Oct-2004
C:Accession: A23132
R:Wierow, G.J.; Lieberman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.; F
J. Cell Biol. 107, 2729-2736, 1988
A:Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struct
A:Reference number: A92750; MUID:89079778; PMID:2462567
A:Accession: A23132
A:Molecule type: mRNA
A:Residues: 1-434 <NIS>
A:Cross-references: UNIPROT:P19140; UNIPARC:UPI00001711A5; GB:X14195; NID:g62455; PIDN:C
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
      ||||| ||||| |||||
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 16
A24742
phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat
N:Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 05-Oct-2004
C:Accession: A24742; PQ0006
R:Sakimura, K.; Kushiya, E.; Obinata, M.; Odani, S.; Takahashi, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
A:Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific enola
A:Reference number: A24742; MUID:86042683; PMID:2865729
A:Accession: A24742
A:Molecule type: mRNA
A:Residues: 1-434 <SAK>
A:Cross-references: UNIPROT:P07323; UNIPARC:UPI00001684CA; GB:M11931; NID:g204041; PIDN:
R:Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y.
Gene 60, 103-113, 1987
A:Title: The structure and expression of neuron-specific enolase gene.
A:Reference number: PQ0006; MUID:88152493; PMID:2450052
A:Accession: PQ0006
A:Molecule type: DNA
A:Residues: 1-28 <SA2>
A:Cross-references: UNIPARC:UPI000014B62B; GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
      ||||| ||||| |||||
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 17
A23126
phosphopyruvate hydratase (EC 4.2.1.11) alpha - rat
N:Alternate names: enolase alpha; nonneuronal enolase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 05-Oct-2004
C:Accession: A23126
R:Sakimura, K.; Kushiya, E.; Obinata, M.; Takahashi, Y.
. . . . .

Nucleic Acids Res. 13, 4365-4378, 1985
A:Title: Molecular cloning and the nucleotide sequence of cDNA to mRNA for non-neuronal
A:Reference number: A23126; MUID:85242108; PMID:289793
A:Accession: A23126
A:Molecule type: mRNA
A:Residues: 1-434 <SAK>
A:Cross-references: UNIPROT:P04764; UNIPARC:UPI000015C86D; GB:X02610; NID:g56106; PIDN
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
      ||||| ||||| |||||
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 18
T25040
hypothetical protein T21B10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25040
R:Baynes, C.
Submitted to the EMBL Data Library, December 1995
A:Reference number: Z19973
A:Accession: T25040
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-434 <Ntl>
A:Cross-references: UNIPROT:Q27527; UNIPARC:UPI0000164061; EMBL:Z68318; PIDN:CAA92692.1
A:Experimental source: clone T21B10
C:Genetics:
A:Gene: CBSP:T21B10.2
A:Map position: 2
A:Introns: 29/1; 344/3
C:Superfamily: enolase

Query Match      62.2%; Score 56; DB 2; Length 434;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
      ||||| ||||| |||||
Db      385 LVVGLATGQIKTGAPC 400

RESULT 19
S07586
phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly (Drosophila melanogaster)
N:Alternate names: enolase
C:Species: Drosophila melanogaster
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S07586
R:Bishop, J.G.; Corces, V.G.
Nucleic Acids Res. 18, 191, 1990
A:Title: The nucleotide sequence of a Drosophila melanogaster enolase gene.
A:Reference number: S07586; MUID:90174924; PMID:2106662
A:Accession: S07586
A:Molecule type: DNA
A:Residues: 1-433 <Bis>
A:Cross-references: UNIPROT:P15007; UNIPARC:UPI0000129F6C; EMBL:X17034; NID:g7945; PIDN
C:Genetics:
A:Gene: FlyBase:Eno
A:Cross-references: FlyBase:FBgn0000579
A:Map position: 22A
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      61.1%; Score 55; DB 2; Length 433;
Best Local Similarity 75.0%; Pred. No. 0.49;
```

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 LVGLCTCQIKTGAPC 16  
Db 385 LVGLSTGQIKTGAPC 400

## RESULT 20

A33850  
phosphorylase hydratase (EC 4.2.1.11), skeletal muscle - chicken  
N:Alternate names: enolase, skeletal muscle  
C:Species: Gallus gallus (chicken)  
C>Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 05-Oct-2004  
C:Accession: A23850; A60809  
R:Russett, G.A.; Dunbar, B.; Fochergill-Gilmore, L.A.  
Biochem. J. 236, 115-126, 1986  
A:Title: The complete amino acid sequence of chicken skeletal-muscle enolase.  
A:Reference number: A23850; MUID:87075592; PMID:3539098  
A:Accession: A23850  
A:Molecule type: protein  
A:Residues: 1-433 <RUS>  
A:Cross-references: UNIPROT:P07322; UNIPARC:UPI0000176060  
R:Gibson, B.W.; Daley, D.J.; Williams, D.H.  
Anal. Biochem. 169, 217-226, 1988  
A:Title: Structural elucidation of N-terminal post-translational modifications by mass  
A:Reference number: A60809; MUID:88250539; PMID:2898218  
A:Accession: A60809  
A:Molecule type: protein  
A:Residues: 1-9 <GIB>  
A:Cross-references: UNIPARC:UPI0000176061  
C:Comment: Several tissue-specific enolase isoenzymes are found in vertebrates.  
C:Superfamily: enolase  
C:Keywords: acetylated amino end; carbon-oxygen lyase; gluconeogenesis; glycolysis; hydr

F1/Modified site: acetylated amino end (Ser) #status experimental  
F13/Binding site: magnesium 2 (Ser) #status predicted  
F1209/Active site: Glu #status predicted  
F1244,292,317/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 61.1%; Score 55; DB 2; Length 433;  
Best Local Similarity 68.8%; Pred. No. 0.49;

Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LVGLCTCQIKTGAPC 16  
Db 383 LVGLCTGQIKTGAPC 398

## RESULT 21

A53665  
phosphorylase hydratase (EC 4.2.1.11) - liver fluke  
C:Species: Fasciola hepatica (liver fluke)  
C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 05-Oct-2004  
C:Accession: A53665  
R:David, R.E.; Singh, H.; Bocka, C.; Hardwick, C.; Ashraf el Mennawy, M.; Villanueva, J.  
J. Biol. Chem. 269, 20026-20030, 1994  
A:Title: RNA trans-splicing in Fasciola hepatica. Identification of a spliced leader (SL)  
A:Reference number: A53665; MUID:94327554; PMID:8051087  
A:Accession: A53665  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-431 <DAV>  
A:Cross-references: UNIPARC:UPI0000176070; GB:U10297; NID:9499266; PIDN:AAA57450.1; PID:  
C:Superfamily: enolase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 58.9%; Score 53; DB 2; Length 431;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LVGLCTCQIKTGAPC 16  
Db 384 LVGLRTGQIKTGAPC 399

## RESULT 22

T03267  
probable phosphorylase hydratase (EC 4.2.1.11) - rice  
N:Alternate names: 2-phospho-D-glycerate hydrolase; enolase  
C:Species: Oryza sativa (rice)  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T03267  
R:Hsing, Y.C.  
submitted to the EMBL Data Library, May 1994  
A:Reference number: Z14869  
A:Accession: T03267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-446 <HSI>  
A:Cross-references: UNIPROT:Q42971; UNIPARC:UPI0000129F87; EMBL:U09450; NID:9780371; P  
A:Experimental source: strain Tainung 67  
C:Function:  
A:Description: catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate  
C:Superfamily: enolase  
C:Keywords: carbon-oxygen lyase; glycolysis; hydro-lyase

Query Match 57.8%; Score 52; DB 2; Length 446;  
Best Local Similarity 68.8%; Pred. No. 1.5;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LVGLCTCQIKTGAPC 16  
Db 395 LVGLATGQIKTGAPC 410

## RESULT 23

J01186  
phosphorylase hydratase (EC 4.2.1.11) - tomato (fragment)  
N:Alternate names: enolase  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: J01186  
R:Van Der Straeten, D.; Rodrigues-Pousada, R.A.; Goodman, H.M.; Van Montagu, M.  
Plant Cell 3, 719-735, 1991  
A:Title: Plant enolase: gene structure, expression, and evolution.  
A:Reference number: J01185; MUID:93044507; PMID:1841726  
A:Accession: J01186  
A:Molecule type: DNA  
A:Residues: 1-326 <VAN>  
A:Cross-references: UNIPROT:Q42887; UNIPARC:UPI00009E691; EMBL:X58109; NID:919205; PID  
C:Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phosph  
C:Genetics:  
A:Introns: 27/3; 61/3; 88/3; 113/3; 134/3; 160/3; 225/3; 242/3; 272/2; 289/3; 308/3  
C:Superfamily: enolase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 326;  
Best Local Similarity 68.8%; Pred. No. 1.6;  
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LVGLCTCQIKTGAPC 16  
Db 283 LVGLSTGQIKTGAPC 298

## RESULT 24

J01185  
phosphorylase hydratase (EC 4.2.1.11) - tomato  
N:Alternate names: enolase  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: J01185; S18191  
R:Van Der Straeten, D.; Rodrigues-Pousada, R.A.; Goodman, H.M.; Van Montagu, M.  
Plant Cell 3, 719-735, 1991  
A:Title: Plant enolase: gene structure, expression, and evolution.  
A:Reference number: J01185; MUID:93044507; PMID:1841726

A:Accession: J01185  
A:Molecule type: mRNA  
A:Residues: 1-444 <VAN>  
A:Cross-references: UNIPROT:P26300; UNIPARC:UPI00000129F6; EMBL:X58108; NID:g19280; PIRN  
A:Experimental source: cv. Orlando  
A:Note: Introns in the coding regions for residues 1-110 and 437-444 are not revealed  
C:Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phospho  
C:Gene: eno2  
A:Introns: 110/3; 137/3; 171/3; 198/3; 223/3; 244/3; 270/3; 335/3; 352/3; 382/2; 399/3;  
C:Superfamily: enolase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 444;  
Best Local Similarity 68.8%; Pred. No. 2.1;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
DB 393 LAVGLSTGQIKTGAPC 408

## RESULT 25

J01187

phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana

N:Alternate names: enolase

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C:Accession: J01187; F84781

R:Van Der Straeten, D.; Rodrigues-Fonseca, R.A.; Goodman, H.M.; Van Montagu, M.

Plant Cell 3, 719-735, 1991

A:Title: Plant enolase: gene structure, expression, and evolution.

A:Reference number: J01185; MUID:93044507; PMID:1841726

A:Accession: J01187

A:Molecule type: DNA

A:Residues: 1-444 <VAN>

A:Cross-references: UNIPROT:P25696; UNIPARC:UPI0000000D31; EMBL:X58107; NID:g16270; PIRN

M.; Rilt, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-444 <STO>

A:Cross-references: UNIPARC:UPI0000000D31; GB:AE002093; NID:g458151; PIRN:AA024635.1; C

C:Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phospho

A:Gene: At2g36530

A:Map position: 2

A:Introns: 22/3; 65/3; 81/3; 110/3; 137/3; 198/3; 244/3; 270/3; 335/3; 399/3; 418/3

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 444;  
Best Local Similarity 68.8%; Pred. No. 2.1;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
DB 393 LAVGLSTGQIKTGAPC 408

## RESULT 26

T02221

phosphopyruvate hydratase (EC 4.2.1.11) - maize

N:Alternate names: enolase

C:Species: Zea mays (maize)

C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004

C:Accession: T02221

R:Pal, S.K.; Lee, C.; Sachs, M.M.

Plant Physiol. 118, 1285-1293, 1998

A:Title: Differential regulation of enolase during anaerobiosis in maize.

A:Reference number: Z14628; MUID:99063764; PMID:9847102

A:Accession: T02221

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-446 <LAL>

A:Cross-references: UNIPROT:P42895; UNIPARC:UPI0000129F41; EMBL:U17973; NID:g602252; PIR

A:Experimental source: strain B73Ht; roots

C:Gene: eno2

C:Function:

A:Description: catalyzes the reversible dehydration of 2-phospho-D-glycerate to phospho

C:Superfamily: enolase

F:43/Binding site: magnesium 2 (ser) #status predicted

F:216/354/Active site: Glu, Lys #status predicted

F:251/302/Binding site: magnesium 1 (asp, Glu, asp) #status predicted

Query Match 56.7%; Score 51; DB 2; Length 446;  
Best Local Similarity 68.8%; Pred. No. 2.1;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
DB 395 LAVGLSTGQIKTGAPC 410

## RESULT 27

S39203

phosphopyruvate hydratase (EC 4.2.1.11) - caenor bean

N:Alternate names: enolase

C:Species: Ricinus communis (castor bean)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S39203

R:Blakeley, S.D.; Cole, K.C.; Dennis, D.T.

submitted to the EMBL Data Library, November 1993

A:Description: Isolation of a full length cDNA clone encoding cytosolic enolase from Ri

A:Reference number: S39203

A:Accession: S39203

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-445 <BLA>

A:Cross-references: UNIPROT:P42896; UNIPARC:UPI0000129F92; EMBL:Z28386; NID:g433608; PIR

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.6%; Score 50; DB 2; Length 445;  
Best Local Similarity 68.8%; Pred. No. 3;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16  
DB 394 LSVGLATGQIKTGAPC 409

## RESULT 28

T12341

phosphopyruvate hydratase (EC 4.2.1.11) - common ice plant

N:Alternate names: 2-phospho-D-glycerate hydratase; enolase

C:Species: Mesembryanthemum crystallinum (common ice plant)

C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004

C:Accession: T12341

R:Forsthoefel, N.R.; Cushman, M.F.; Cushman, J.C.

submitted to the EMBL Data Library, April 1994

A:Description: Characterization and stress-induced expression of enolase from the facult

A:Accession: T12341

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-444 <FOR>

A:Cross-references: UNIPROT:Q43130; UNIPARC:UPI000016D5B; EMBL:U09194; NID:g533473; PIR



A:Description: catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 444;  
 Best Local Similarity 68.8%; Pred. No. 4.3;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 393 LSVGLSTGQIKTGAPC 408

## RESULT 29

S16257  
 phosphopyruvate hydratase (EC 4.2.1.11) - maize  
 N:Alternate names: enolase  
 C:Species: Zea mays (maize)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S16257  
 R:Lat. S.K.: Johnson, S.; Conway, T.; Kelley, P.M.  
 Plant Mol. Biol. 16, 787-795, 1991  
 A:Title: Characterization of a maize cDNA that complements an enolase-deficient mutant C  
 A:Reference number: S16257; MUID:91316216; PMID:1859865  
 A:Accession: S16257  
 A:Molecule type: mRNA  
 A:Residues: 1-446 <LAL>  
 A:Cross-references: UNIPROT:P26301; UNIPARC:UPI0000129F3D; EMBL:X55981; NID:g22272; PIDN  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 446;  
 Best Local Similarity 68.8%; Pred. No. 4.3;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 395 LSVGLSTGQIKTGAPC 410

## RESULT 30

S24996  
 phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas reinhardtii  
 N:Alternate names: enolase  
 C:Species: Chlamydomonas reinhardtii  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S24996  
 R:Dumont, F.  
 submitted to the EMBL Data Library, May 1992  
 A:Reference number: S24989  
 A:Accession: S24996  
 A:Molecule type: mRNA  
 A:Residues: 1-372 <DDU>  
 A:Cross-references: UNIPROT:P31683; UNIPARC:UPI0000129F64; EMBL:X66412; NID:gl0142; PIDN  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 53.3%; Score 48; DB 2; Length 372;  
 Best Local Similarity 62.5%; Pred. No. 5.3;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 323 LAVGLASGQIKTGAPC 338

Search completed: April 3, 2006, 08:04:35  
 Job time : 17 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:02:35 ; Search time 56 Seconds  
(without alignments)  
201.580 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVGLCTCQIKTPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	82.2	458	1	ENO1B_HUMAN
2	68	75.6	433	1	ENO4 BOVIN
3	65	72.2	88	2	Q804Y6 ICTPU
4	65	72.2	154	2	Q9NPL4_HUMAN
5	65	72.2	159	2	Q9NG70_9BILA
6	65	72.2	184	2	Q96GV1_HUMAN
7	65	72.2	259	2	Q7Z2M5_SPAUV
8	65	72.2	272	2	Q9BT62_HUMAN
9	65	72.2	338	2	Q922A0_MOUSE
10	65	72.2	366	2	Q6PHC1_MOUSE
11	65	72.2	377	2	Q6LDC3_ANAPL
12	65	72.2	383	2	Q9NG67_9HEXA
13	65	72.2	394	2	Q9PTX6_LAMRE
14	65	72.2	395	1	ENO_ALIMI
15	65	72.2	395	2	Q9U5F7_EPTBU
16	65	72.2	395	2	Q9PTX5_LAMRE
17	65	72.2	406	2	Q4SZW2_TETNG
18	65	72.2	420	2	Q5ISQ0_MACFA
19	65	72.2	431	2	Q4TBD1_TETNG
20	65	72.2	432	2	Q6T0P5_BRARE
21	65	72.2	432	2	Q6FC12_BRARE
22	65	72.2	433	1	ENO_ALIMI
23	65	72.2	433	1	ENO_ANAPL
24	65	72.2	433	1	ENO_CHICK
25	65	72.2	433	1	ENO_MOUSE
26	65	72.2	433	1	ENO_HUMAN
27	65	72.2	433	1	ENO_PYTRG
28	65	72.2	433	1	ENO_RAT
29	65	72.2	433	1	ENO_SCEUN
30	65	72.2	433	1	ENO_TRASC
31	65	72.2	433	1	ENO_CHICK

32	65	72.2	433	1	ENO_HUMAN	P13929 homo sapien
33	65	72.2	433	1	ENO_MOUSE	P21550 mus musculu
34	65	72.2	433	1	ENO_RABIT	P25704 oryctolagus
35	65	72.2	433	1	ENO_RAT	P15429 rattus norv
36	65	72.2	433	1	ENO_HUMAN	P09104 homo sapien
37	65	72.2	433	1	ENO_MOUSE	P07323 rattus norv
38	65	72.2	433	1	ENO_RAT	P56522 homarus gam
39	65	72.2	433	1	ENO_HOMGA	P08734 xenopus lae
40	65	72.2	433	1	ENO_XENIA	P06C89 brachydanio
41	65	72.2	433	2	Q6FC89_BRARE	Q6TH14 brachydanio
42	65	72.2	433	2	Q6TH14_BRARE	Q568G3 brachydanio
43	65	72.2	433	2	Q568G3_BRARE	Q02654 loligo peal
44	65	72.2	434	1	ENO_LOLPE	P33676 schistosoma
45	65	72.2	434	1	ENO_SCHUA	Q27877 schistosoma
46	65	72.2	434	2	Q6FIVE_HUMAN	Q6FIVE_HUMAN
47	65	72.2	434	2	Q4TUS4_HUMAN	Q4TUS4_HUMAN
48	65	72.2	434	2	Q53HR3_HUMAN	Q53HR3_HUMAN
49	65	72.2	434	2	Q53FTE_HUMAN	Q53FTE_HUMAN
50	65	72.2	434	2	Q96656_PENMO	Q96656 penaeus mon
51	65	72.2	434	2	Q5XIV3_RAT	Q5XIV3 rattus norv
52	65	72.2	434	2	Q5DIJ3_SCHUA	Q5DIJ3 SCHUA
53	65	72.2	434	2	Q5DDV5_SCHUA	Q5DDV5 SCHUA
54	65	72.2	434	2	Q5R6Y1_PONPY	Q5R6Y1 pongo pygma
55	65	72.2	434	2	Q4R5L2_MACFA	Q4R5L2 macaca fasc
56	65	72.2	434	2	Q5SX58_MOUSE	Q5SX58 mus musculu
57	65	72.2	434	2	Q5XIV3_RAT	Q5XIV3 rattus norv
58	65	72.2	434	2	Q545V3_MOUSE	Q545V3 mus musculu
59	65	72.2	434	2	Q5FW97_MOUSE	Q5FW97 mus musculu
60	65	72.2	434	2	Q4FKS5_MOUSE	Q4FKS5 mus musculu
61	65	72.2	434	2	Q8JFEO_CROPL	Q8JFEO crocodylus
62	65	72.2	434	2	Q7ZXAX_XENIA	Q7ZXAX xenopus lae
63	65	72.2	434	2	Q8AVT0_XENIA	Q8AVT0 xenopus lae
64	65	72.2	434	2	Q6GOM6_BRARE	Q6GOM6 brachydanio
65	65	72.2	434	2	Q7S2Z5_XENIA	Q7S2Z5 xenopus lae
66	65	72.2	434	2	Q4VA70_XENTRA	Q4VA70 xenopus tro
67	65	72.2	434	2	Q4RXG6_TETNG	Q4RXG6 tetraodon n
68	65	72.2	436	2	Q5DCP8_SCHUA	Q5DCP8 schistosoma
69	65	72.2	458	2	Q5XK81_MOUSE	Q5XK81 mus musculu
70	65	72.2	462	2	Q5XUG8_MOUSE	Q5XUG8 mus musculu
71	65	72.2	463	2	Q4QR91_RAT	Q4QR91 rattus norv
72	65	72.2	464	2	Q5BJ93_RAT	Q5BJ93 rattus norv
73	65	72.2	464	2	Q5EB49_RAT	Q5EB49 rattus norv
74	61	67.8	387	2	Q5WQI5_PHATRA	Q5WQI5 pheodactyl
75	61	67.8	389	2	Q5WQW2_9STRA	Q5WQW2 heterosigma
76	61	67.8	430	2	Q5U0Y7_HETTR	Q5U0Y7 heterocarpa
77	59	65.6	434	1	ENO_CHICK	Q5J391 gallus galli
78	58	64.4	251	2	Q9NG71_LIMPO	Q9NG71 limulus pol
79	56	62.2	337	2	Q814F9_CABEL	Q814F9 caenorhabdi
80	56	62.2	433	1	ENO_CABEL	Q27527 caenorhabdi
81	56	62.2	434	2	Q61Z94_CABER	Q61Z94 caenorhabdi
82	56	62.2	437	2	Q67U00_TRISP	Q67U00 trichinella
83	56	62.2	465	2	Q6A4N1_CABEL	Q6A4N1 caenorhabdi
84	55	61.1	159	2	Q9NG73_9HEXA	Q9NG73 euneosocampa
85	55	61.1	358	2	Q56RP1_DROAI	Q56RP1 dirosophila
86	55	61.1	371	2	Q967N8_9CUCU	Q967N8 hyocoryphal
87	55	61.1	373	2	Q56RN8_DROMI	Q56RN8 dirosophila
88	55	61.1	384	2	Q9NG68_9MYRI	Q9NG68 scolopendra
89	55	61.1	409	2	Q56RP2_DROMI	Q56RP2 dirosophila
90	55	61.1	409	2	Q56RN2_DROMI	Q56RN2 dirosophila
91	55	61.1	413	2	Q44100_DROPS	Q44100 dirosophila
92	55	61.1	413	2	Q44101_DROSU	Q44101 dirosophila
93	55	61.1	433	2	Q7QJDB_ANOGA	Q7QJDB anopheles g
94	55	61.1	433	2	Q5XKS5_9HEMI	Q5XKS5 oncomelasma
95	55	61.1	442	2	Q4NIN1_THEIPA	Q4NIN1 theileria p
96	55	61.1	442	2	Q4UBV7_THEAN	Q4UBV7 theileria a
97	55	61.1	500	1	ENO_DROME	P15007 dirosophila
98	53	58.9	433	1	ENO_PASHE	Q27655 fasciola he
99	53	58.9	433	2	Q93873_PNECA	Q93873 pneumocystis
100	53	58.9	434	2	Q54RK5_DICDI	Q54RK5 dictyosteli

ALIGNMENTS

```

RESULT 1
ENOB1_HUMAN STANDARD; PRT; 458 AA.
ID ENOB1_HUMAN STANDARD; PRT; 458 AA.
AC Q05524;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase, lung specific (EC 4.2.1.11) (2-phospho-D-glycerate
hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase)
DE (HLE1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung fibroblast;
RX MEDLINE=93372640; PubMed=7689884;
RA Verma M., Kuri R.N.;
RT "Human lung enolase: cloning and sequencing of cDNA and its
inducibility with dexamethasone."
RL Biochem. Mol. Biol. Int. 30:293-303 (1993).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
the dimer.
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- INDUCTION: By dexamethasone.
CC -1- SIMILARITY: Belongs to the enolase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X66610; CAA47179.1; -; mRNA.
DR PIR; I37360; I37360.
DR HSSP; P56252; 1PDZ.
DR Reactome; Q05524; -.
DR MIM; 607098; -.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; TAS.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAmE; TIGR01060; eno; 1.
DR KEGG; K00001; Enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GlycoLyse; Lyase; Magnesium; Metal-binding; Multigene family.
FT ACT SITE 167
FT METAL 254 254 Magnesium (By similarity).
FT METAL 308 308 Magnesium (By similarity).
FT METAL 336 336 Magnesium (By similarity).
SQ SEQUENCE 458 AA; 49477 MW; 2590F34A28F44314 CRC64;

Query Match 82.2%; Score 74; DB 1; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0017;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LVVGLCTQIXTGPAC 16
Db 407 LVVGLCTQIXTGPAC 422

```

RESULT 2  
ENOB\_BOVIN

```

ID ENOB_BOVIN STANDARD; PRT; 433 AA.
AC Q9XSJ4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-
neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (HAP47).
GN Name=ENO1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chapman K.T., Newman B., Hillyard M.C., Freemont A.J., Grant M.E.,
RA Boot-Handford R., Wallis G.A.;
RT "Alpha enolase is upregulated in proliferative chondrocytes in the
epiphyseal growth plate and in human osteoarthritic tissue."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE OF 269-280 AND 372-393, AND FUNCTION AS AN
RP ENDOTHELIAL HYPOXIC STRESS PROTEIN.
RX MEDLINE=96070906; PubMed=7499243; DOI=10.1074/jbc.270.46.2752;
RA Aronson R.M., Graven K.K., Tucci M., McDonald R.J., Farber H.W.;
RT "Non-neuronal enolase is an endothelial hypoxic stress protein."
RL J. Biol. Chem. 270:2752-2757 (1995).
CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in
glycolysis, plays a part in various processes such as growth
control, hypoxia tolerance and allergic responses. May also
function in the intravascular and pericellular fibrolytic system
due to its ability to serve as a receptor and activator of
plasminogen on the cell surface of several cell-types such as
leucocytes and neurons (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,
alpha, beta and gamma, which can form homodimers or heterodimers
which are cell-type and development-specific. ENO1 interacts with
PLG in the neuronal plasma membrane and promotes its activation.
The C-terminal lysine is required for this binding (By
similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma
membrane in either the homodimeric (alpha/alpha) or heterodimeric
(alpha/gamma) form (By similarity). ENO1 is localized to the M-
band (By similarity).
CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in
embryo and in most adult tissues. The alpha/beta heterodimer and
the beta/beta homodimer are found in striated muscle, and the
alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.
CC -1- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition
from the alpha/alpha homodimer to the alpha/beta heterodimer in
striated muscle cells, and to the alpha/gamma heterodimer in nerve
cells.
CC -1- INDUCTION: Expression increased up to 3-fold by hypoxic stress in
vascular endothelial cells.
CC -1- SIMILARITY: Belongs to the enolase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF149256; AAD33073.1; -; mRNA.
DR HSSP; Q9NDH8; 1OEP.
DR SMR; Q9XSJ4; 1-430.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.

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DR Pfam; PF03952; Enolase N; 1.  
 DR PRINTS; PRO0148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRfam; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 KW Direct protein sequencing; Glycolysis; Lyase; Magnesium;  
 KW Metal-binding; Multigene family; Plasmidogen activation.  
 FT INIT MET 0  
 FT REGION 404 433  
 FT ACT SITE 157 157  
 FT METAL 244 244  
 FT METAL 292 292  
 FT METAL 317 317  
 SQ SEQUENCE 433 AA; 47146 MW; B004E965C46F2E0C CRC64;  
 Query Match 75.6%; Score 68; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.015;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 1 LVVGLCTGQIKTGAPC 16  
 383 LVVGLCTGQIKTGAPC 398  
 RESULT 3  
 O804Y6 ICTPU  
 ID O804Y6 ICTPU PRELIMINARY; PRT; 88 AA.  
 AC O804Y6;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Enolase (Fragment).  
 OS Ictalurus punctatus (Channel catfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
 OC Ictaluridae; Ictalurus.  
 OX NCBI\_TaxId=7998;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Muscle;  
 RA Kim S., Li P., Zheng X., Dunham R.A., Liu Z.;  
 RT "Gene expression in the muscles of young and mature channel catfish  
 RT (Ictalurus punctatus) as analyzed by expressed sequence tags and gene  
 RT filters.";  
 RL Fish Physiol. Biochem. 0:0-0(2003).  
 DR EMBL; AF227804; AAO25761.1; -; mRNA.  
 DR HSSP; P56252; 1PDZ.  
 DR SMR; O804Y6; 4-85.  
 DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
 DR GO; GO:0016823; F:lyase activity; IEA.  
 DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro; IPR000941; Enolase.  
 DR Pfam; PF00113; Enolase C; 1.  
 DR ProDom; PD000902; Enolase; 1.  
 FT NON TER 1  
 FT SEQUENCE 88 AA; 9830 MW; 8C14B5E5FDB836C1 CRC64;  
 Query Match 72.2%; Score 65; DB 2; Length 88;  
 Best Local Similarity 81.2%; Pred. No. 0.011;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 1 LVVGLCTGQIKTGAPC 16  
 38 LVVGLCTGQIKTGAPC 53

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Auffray C., Ansoorge W., Ballabio A., Estivill X., Gibson K.,  
 RA Lehrach H., Poustka A., Lundberg J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Andreu N., Estivill X., Escarceller M., Suney L.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 DR EMBL; AL359213; CAB94588.1; -; mRNA.  
 DR HSSP; P56252; 1PDZ.  
 DR SMR; O9NPL4; 1-151.  
 DR Ensemble; ENSG00000108515; Homo sapiens.  
 DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
 DR GO; GO:0016823; F:lyase activity; IEA.  
 DR GO; GO:0000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro; IPR000941; Enolase.  
 DR Pfam; PF00113; Enolase C; 1.  
 DR PRINTS; PRO0148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 KW Glycolysis; Lyase; Magnesium.  
 FT NON TER 1  
 FT SEQUENCE 154 AA; 16939 MW; 347B95809B1C864D CRC64;  
 Query Match 72.2%; Score 65; DB 2; Length 154;  
 Best Local Similarity 81.2%; Pred. No. 0.019;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Db 1 LVVGLCTGQIKTGAPC 16  
 104 LVVGLCTGQIKTGAPC 119  
 RESULT 5  
 O9NG70 9BILA  
 ID O9NG70 9BILA PRELIMINARY; PRT; 159 AA.  
 AC O9NG70;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Enolase (Fragment).  
 OS Peripatus sp. Per3.  
 OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.  
 OX NCBI\_TaxId=126380;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Regier J.C., Shultz J.W.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.

```
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: AF258667; AAF72638.1; -; mRNA.
DR HSSP: P56252; 1PDZ.
DR SMR: Q9NG70; 1-159.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006036; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C_1.
DR PRINTS: PR00148; ENOLASE.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT TER 159
SQ SEQUENCE 159 AA; 17583 MW; 840E266ACD36D3CD CRC64;

Query Match 72.2%; Score 65; DB 2; Length 159;
Best Local Similarity 81.2%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 138 LVVGLCTGQIKTGAPC 153

RESULT 6
096GV1 HUMAN PRELIMINARY; PRT; 184 AA.
AC 096GV1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ENO1 protein (Fragment).
GN Name=ENO1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.S.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maitra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RC Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
-1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
```

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CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC009218; AA09218.2; -; mRNA.
DR HSSP: P56252; 1PDZ.
DR SMR: Q96GV1; 1-181.
DR Ensembl: ENSG0000074800; Homo sapiens.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006036; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C_1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 184 AA; 20415 MW; F94E113824E5290A CRC64;

Query Match 72.2%; Score 65; DB 2; Length 184;
Best Local Similarity 81.2%; Pred. No. 0.022;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 134 LVVGLCTGQIKTGAPC 149

RESULT 7
072ZM5 SPANU PRELIMINARY; PRT; 259 AA.
AC 072ZM5;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Sparus.
NCBI_TaxID=8175;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RA Ribes L., Planas J.V., Monetti C., Bernardini G., Saroglia M.,
RA Tort L., Mackenzie S.;
RT "A differentially expressed enolase gene isolated from the gilthead
RT sea bream (Sparus aurata) under high-density conditions is up-
RT regulated in brain after in vivo lipopolysaccharide challenge."
RL Aquaculture 241:195-206 (2004).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- PATHWAY: Glycolysis.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: AY263379; AA092646.1; -; mRNA.
DR HSSP: P56252; 1PDZ.
DR SMR: Q7ZM5; 2-258.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006036; P:glycolysis; IEA.
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DR InterPro: IPR000941; Enolase.  
DR Pfam: PF00113; Enolase C; 1.  
DR PRINTS: PR00148; ENOLASE.  
DR PRODOM: PD000902; ENOLASE; 1.  
DR PROSITE: PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON TER 1  
FT NON TER 259  
SQ SEQUENCE 259 AA; 26484 MW; 1DE915D3B95531B CRC64;  
  
Query Match 72.2%; Score 65; DB 2; Length 259;  
Best Local Similarity 81.2%; Pred. No. 0.03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 LVVGLCTGQIKTGAPC 16  
DB 209 LVVGLCTGQIKTGAPC 224  
  
RESULT 8  
Q9BT62 HUMAN PRELIMINARY; PRT; 272 AA.  
ID Q9BT62;  
AC Q9BT62;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE ENO1 protein (Fragment).  
GN Name=ENO1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullish S.J.,  
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
H(2)O.  
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
the dimer (By similarity).  
CC -1- PATHWAY: Glycolysis.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the enolase family.  
DR EMBL: BC004325; AA04325.1; -; mRNA.  
DR HSSP: P56252; 1pD2.  
DR SMR: Q9BT62; 1-269.
```

```
DR Ensemble: ENSG00000074800; Homo sapiens.  
DR GO: GO:0006015; C:phosphopyruvate hydratase complex; IEA.  
DR GO: GO:0016823; F:lyase activity; IEA.  
DR GO: GO:0000287; F:magnesium ion binding; IEA.  
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR GO: GO:0006096; P:glycolysis; IEA.  
DR InterPro: IPR000941; Enolase.  
DR Pfam: PF00113; Enolase C; 1.  
DR PRINTS: PR00148; ENOLASE.  
DR PRODOM: PD000902; ENOLASE; 1.  
DR PROSITE: PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON TER 1  
FT NON TER 259  
SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88DDC CRC64;  
  
Query Match 72.2%; Score 65; DB 2; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 LVVGLCTGQIKTGAPC 16  
DB 222 LVVGLCTGQIKTGAPC 237  
  
RESULT 9  
Q922A0 MOUSE PRELIMINARY; PRT; 338 AA.  
ID Q922A0;  
AC Q922A0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Eno2 protein (Fragment).  
GN Name=Eno2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Mammary tumor. C3;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullish S.J.,  
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
H(2)O.  
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
the dimer (By similarity).  
CC -1- PATHWAY: Glycolysis.  
CC -1- SUBUNIT: Homodimer (By similarity).
```

```
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC009018; AA09018.1; -; mRNA.
DR HSSP: P56252; 1PD2.
DR SMR: Q922A0; 25-143, 125-338.
DR Ensembl: ENSMUSG00000004267; Mus musculus.
DR MGI: MGI:95394; Eno2.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0000287; F:magnesium ion binding; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR Prodom: PD000902; Enolase_N; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium.
FT NON_TER
SQ SEQUENCE 338 AA; 37146 MW; B0F2F321D749484 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 338;
Best Local Similarity 81.2%; Pred. No. 0.038;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
Db 288 LVVGLCTGQIKTGAPC 303

RESULT 10
ID Q6PHCL_MOUSE PRELIMINARY; PRT; 366 AA.
AC Q6PHCL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Eno1 protein.
GN Name=Eno1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toohiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RN Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
```

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DR EMBL: BC056611; AA056611.1; -; mRNA.
DR SMR: Q6PHCL; 3-363.
DR MGI: MGI:95393; Enol.
DR GO: GO:0005515; F:protein binding; TAS.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR Pfam: PF03952; Enolase_N; 1.
DR PRINTS: PR00148; ENOLASE.
DR Prodom: PD000902; Enolase; 1.
DR TIGRFAMs: TIGR01060; eno; 1.
DR PROSITE: PS00164; ENOLASE; 1.
SQ SEQUENCE 366 AA; 39782 MW; 11E90DDDE4B67D1 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 0.04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
Db 316 LVVGLCTGQIKTGAPC 331

RESULT 11
ID Q6LDK3_ANAPL PRELIMINARY; PRT; 377 AA.
AC Q6LDK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-enolase/tau-crystallin (EC 4.2.1.11).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89079778; PubMed=2462567; DOI=10.1083/jcb.107.6.2729;
RA Wistow G.J., Lieberman T., Williams L.A., Stapel S.O., de Jong W.W.,
RA Horwitz J., Platiogorsky J.;
RT "Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a
RT lens structural protein.";
J. Cell Biol. 107:2729-2736(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91365245; PubMed=1889745; DOI=10.1016/0378-1119(91)90273-E;
RA Kim R.Y., Belman T., Platiogorsky J., Wistow G.J.;
RT "Structure and expression of the duck alpha-enolase/-tau-crystallin-
RT encoding gene.";
Gene 103:193-200(1991).
RL Gene 103:193-200(1991).
DR EMBL: M55143; AAA49217.1; -; Genomic_DNA.
DR EMBL: M55134; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55135; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55136; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55138; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55140; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55142; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55141; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55139; AAA49217.1; JOINED; Genomic_DNA.
DR EMBL: M55137; AAA49217.1; JOINED; Genomic_DNA.
DR SMR: Q6LDK3; 1-376.
DR GO: GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; Enolase_C; 1.
DR Pfam: PF03952; Enolase_N; 1.
DR PRINTS: PR00148; ENOLASE.
DR Prodom: PD000902; Enolase; 1.
DR TIGRFAMs: TIGR01060; eno; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Lyase.
SQ SEQUENCE 377 AA; 40856 MW; 64B2B35F0C17C0C6 CRC64;
```



Query Match 72.2% Score 65; DB 2; Length 377;  
Best Local Similarity 81.2% Pred. No. 0.042;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 327 LVVGLCTGQIKTGAPC 342

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RESULT 12
Q9NG67_9HEXA PRELIMINARY; PRT; 383 AA.
AC Q9NG67;
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DE Enolase (Fragment).
OS Tomocerus sp. jcxjwsl.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Collembola; Arthropodea;
OC Entomobryidae; Tomoceridae; Tomocerus.
NCBI_Taxid=111305;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Regier J.C., Shultz J.W.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COPOLYMER: Magnesium. Required for catalysis and for stabilizing
the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AF258670; AAF72641.1; -; mRNA.
DR HSSP; P56252; 1PD2.
DR SMR; Q9NG67; 1-383.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; ENOLASE; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 383
SQ SEQUENCE 383 AA; 41326 MW; 4523F005FEA5E579 CRC64;

Query Match 72.2% Score 65; DB 2; Length 383;
Best Local Similarity 81.2% Pred. No. 0.042;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
Db 363 LVVGLCTGQIKTGAPC 378

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
NCBI_Taxid=7753;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes."
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COPOLYMER: Magnesium. Required for catalysis and for stabilizing
the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AB025329; BAA88482.1; -; mRNA.
DR HSSP; P56252; 1PD2.
DR SMR; Q9PTX6; 1-392.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; ENOLASE; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 394
SQ SEQUENCE 394 AA; 42583 MW; BC585FE6C712A3D2 CRC64;

Query Match 72.2% Score 65; DB 2; Length 394;
Best Local Similarity 81.2% Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16
Db 345 LVVGLCTGQIKTGAPC 360

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RESULT 14
EN0_ALIMI STANDARD; PRT; 395 AA.
AC P42897;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
glycerate hydro-lyase) (Fragment).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Crocodyliidae; Alligatorinae; Alligator.
NCBI_Taxid=8496;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94195794; PubMed=8146164;
RA Hedger S.B.;
RT "Molecular evidence for the origin of birds."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COPOLYMER: Magnesium. Required for catalysis and for stabilizing
the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the enolase family.

```

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CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; L28078; AAA53671.1; -, mRNA.
CC PIR; I50026; I50026.
CC HSSP; P56252; 1PDZ.
CC SMK; P42897; 1-395.
CC InterPro; IPR000941; Enolase.
CC PANTHER; PTHR11902; Enolase; 1.
CC Pfam; PF00113; Enolase_C; 1.
CC Pfam; PF03952; Enolase_N; 1.
CC PRINTS; PR00148; ENOLASE.
CC ProDom; PD000902; Enolase; 1.
CC TIGRFAMs; TIGR01060; eno; 1.
CC PROSITE; PS00164; ENOLASE; 1.
CC GLYCOLYSIS; Lyase; Magnesium; Metal-binding.
CC ACT_SITE 136 136
CC METAL 223 223 By similarity.
CC METAL 271 271 Magnesium (By similarity).
CC METAL 296 296 Magnesium (By similarity).
CC NON_TER 1 1
CC NON_TER 395 395
CC SEQUENCE 395 AA; 42884 MW; B43B91228B9110B5 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
Db 362 LVVGLCTGQIKTGAPC 377

RESULT 15
Q9USF7 EPTBU ID Q9USF7 EPTBU PRELIMINARY; PRT; 395 AA.
AC Q9USF7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Eptatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxId=7764;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AB025326; BAA8479.1; -, mRNA.
DR HSSP; P56252; 1PDZ.
DR SMK; Q9USF7; 1-392.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; F:glycolysis; IEA.
```

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DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GLYCOLYSIS; Lyase; Magnesium.
CC ACT_SITE 136 136
CC NON_TER 1 1
CC NON_TER 395 395
CC SEQUENCE 395 AA; 43131 MW; D351C670DDC75CD CRC64;

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
Db 345 LVVGLCTGQIKTGAPC 360

RESULT 16
Q9PTX5 LAMRE ID Q9PTX5 LAMRE PRELIMINARY; PRT; 395 AA.
AC Q9PTX5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enolase-2 (Fragment).
GN Name=enolase-2;
OS Lampetra reissneri (Par Eastern brook lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxId=7753;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AB025330; BAA8483.1; -, mRNA.
DR HSSP; P56252; 1PDZ.
DR SMK; Q9PTX5; 1-394.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; F:glycolysis; IEA.
CC InterPro; IPR000941; Enolase.
CC Pfam; PF00113; Enolase_C; 1.
CC Pfam; PF03952; Enolase_N; 1.
CC PRINTS; PR00148; ENOLASE.
CC ProDom; PD000902; Enolase; 1.
CC TIGRFAMs; TIGR01060; eno; 1.
CC PROSITE; PS00164; ENOLASE; 1.
CC GLYCOLYSIS; Lyase; Magnesium.
CC ACT_SITE 136 136
CC NON_TER 1 1
CC NON_TER 395 395
CC SEQUENCE 395 AA; 43267 MW; 8591D68662DA8544 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
Db 345 LVVGLCTGQIKTGAPC 360
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DB 345 LVVGLCTGQIKTGAPC 360

RESULT 17  
Q4SZW2\_TETNG PRELIMINARY; PRT; 406 AA.

AC Q4SZW2;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Chromosome undetermined SCAF11462, whole genome shotgun sequence.  
GN ORFNames=GSTENG0009644001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
NCBI\_TaxId=99883;  
(1)

RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coucanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
(2)

RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CA0101462; CAF93820.1; -; Genomic DNA.  
SQ SEQUENCE 406 AA; 43712 MW; 18C266C4F923E27D CRC64;

Query Match 72.2%; Score 65; DB 2; Length 406;  
Best Local Similarity 81.2%; Pred. No. 0.044;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 358 LVVGLCTGQIKTGAPC 373

RESULT 18  
OSISO0\_MACPA PRELIMINARY; PRT; 420 AA.

AC OSISO0;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Enolase 2 (Fragment)  
OS Macaca fascicularis (Crisp eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecoidea; Macaca.  
NCBI\_TaxId=9541;  
(1)

RP NUCLEOTIDE SEQUENCE.  
RA Pubmed=15620360; DOI=10.1016/j.cell.2004.11.040;  
RA Doris S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,  
RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.;  
RT "Accelerated evolution of nervous system genes in the origin of Homo  
RT sapiens.";  
RL Cell 119:1027-1040(2004).  
CC -! CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
CC H(2)O.  
CC -! COFACTOR: Magnesium. Required for catalysis and for stabilizing  
CC the dimer (By similarity).  
CC -! PATHWAY: Glycolysis.  
CC -! SUBUNIT: Homodimer (By similarity).  
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -! SIMILARITY: Belongs to the enolase family.  
DR EMBL; AY650330; AAV67362.1; -; mRNA.  
DR SMR; Q51S00; 1-420.  
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR GO; GO:0006096; P:glycolysis; IEA.  
DR InterPro; IPR000941; Enolase.  
DR Pfam; PF00113; Enolase\_C; 1.  
DR Pfam; PF03952; Enolase\_N; 1.  
DR PRINTS; PR00148; ENOLASE.  
DR PRODOM; PD000902; Enolase; 1.  
DR TIGRPFAMs; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 420 AA; 45540 MW; 0FF7DC4035539747 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.046;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 377 LVVGLCTGQIKTGAPC 392

RESULT 19  
Q4TBD1\_TETNG PRELIMINARY; PRT; 431 AA.

AC Q4TBD1;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF7145, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG0003809001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
NCBI\_TaxId=99883;  
(1)

RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coucanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
(2)

RP NUCLEOTIDE SEQUENCE.

```
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (by similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; CAAB01007145; CAF89801.1; -; Genomic_DNA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; eno; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GlycoLyse; Lyase; Magnesium.
FT NON_TER 431 431
SQ SEQUENCE 431 AA; 47111 MW; BFA79F670744BC1 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 431;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 20
Q61OP5_BRARE PRELIMINARY; PRT; 432 AA.
ID Q61OP5_BRARE PRELIMINARY; PRT; 432 AA.
AC Q61OP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enolase 1, (Alpha).
GN ORFNames=zgc:73152;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
```

```
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Submitted MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071359; AAH71359.1; -; mRNA.
DR SMR; Q6PC12; 2-431.
DR ZFIN; ZDB-GENE-030131.6048; zgc:73152.
DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; eno; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR SEQUENCE 432 AA; 47059 MW; F743FC00CD249F6F CRC64;

Query Match 72.2%; Score 65; DB 2; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 21
Q6PC12_BRARE PRELIMINARY; PRT; 432 AA.
ID Q6PC12_BRARE PRELIMINARY; PRT; 432 AA.
AC Q6PC12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enolase 1, (Alpha).
GN ORFNames=zgc:73152;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059511; AAH59511.1; -; mRNA.
DR SMR; Q6PC12; 2-431.
```

DR 2FIN; ZDB-GENE-030131-6048; zgc:73152.  
 DR GO; GO:0000015; C:phosphorylruvate hydratase complex; IEA.  
 DR GO; GO:0004634; F:phosphorylruvate hydratase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro; IPR000941; Enolase.  
 DR Pfam; PF00113; Enolase\_C; 1.  
 DR Pfam; PF03952; Enolase\_N; 1.  
 DR PRINTS; PR00148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRFAMs; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 SQ SEQUENCE 432 AA; 47073 MW; 893A8C6D0CF8EF95 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 432;  
 Best Local Similarity 81.2%; Pred. No. 0.047;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 22  
 ENOA\_ALLMI STANDARD; PRT; 433 AA.  
 ID ENOA\_ALLMI  
 AC Q9PVK2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)  
 DE (Phosphorylruvate hydratase).  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylia; Alligatorinae; Alligator.  
 OX NCBI\_TaxId=8496;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=99439677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;  
 RA Mannen H., Li S.S.-L.,  
 RL "Molecular evidence for a clade of turtles."  
 RL Mol. Phylogenet. Evol. 13:144-148(1999).  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.  
 CC -1- COPFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC -----  
 CC EMBL; AF072586; AAD41643.1; -; mRNA.  
 DR HSSP; P56252; 1P02.  
 DR SMR; Q9PVK2; 1-432.  
 DR InterPro; IPR000941; Enolase.  
 DR PANTHER; PTHR11902; Enolase; 1.  
 DR Pfam; PF00113; Enolase\_C; 1.  
 DR Pfam; PF03952; Enolase\_N; 1.  
 DR PRINTS; PR00148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRFAMs; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.  
 FT INIT\_MET 0  
 FT METAL 244 244 Magnesium (By similarity).  
 FT METAL 292 292 Magnesium (By similarity).  
 FT METAL 317 317 Magnesium (By similarity).

SQ SEQUENCE 433 AA; 47191 MW; CD3DD59FB1EBB3DA CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.047;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
 Db 383 LVVGLCTGQIKTGAPC 398

RESULT 23  
 ENOA\_ANAPL STANDARD; PRT; 433 AA.  
 ID ENOA\_ANAPL  
 AC P19140;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Tau-crystallin).  
 DE crystallin).  
 GN Name=ENO1;  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OX NCBI\_TaxId=8839;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryonic lens;  
 RX MEDLINE=89079778; PubMed=2462567; DOI=10.1083/jcb.107.6.2729;  
 RA Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W., Horvitz J., Platigorsky J.;  
 RT "Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens structural protein."  
 RL J. Cell Biol. 107:2729-2736(1998).  
 CC -1- FUNCTION: Both an enzyme and a lens structural protein.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.  
 CC -1- COPFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC -----  
 CC EMBL; M20749; AAA49218.1; -; mRNA.  
 DR EMBL; X14195; CAA32409.1; -; mRNA.  
 DR PIR; A32132; A32132.  
 DR HSSP; P56252; 1P02.  
 DR SMR; P19140; 1-432.  
 DR InterPro; IPR000941; Enolase.  
 DR PANTHER; PTHR11902; Enolase; 1.  
 DR Pfam; PF00113; Enolase\_C; 1.  
 DR Pfam; PF03952; Enolase\_N; 1.  
 DR PRINTS; PR00148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRFAMs; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 KW Eye lens protein; Glycolysis; Lyase; Magnesium; Metal-binding.  
 FT INIT\_MET 0  
 FT ACT\_SITE 157 157 By similarity.  
 FT METAL 244 244 Magnesium (By similarity).  
 FT METAL 292 292 Magnesium (By similarity).  
 FT METAL 317 317 Magnesium (By similarity).  
 SQ SEQUENCE 433 AA; 47109 MW; 1AED7B08A6E84D CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.047;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

## RESULT 24

ENOA\_CHICK STANDARD; PRT; 433 AA.

AC P51913.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE 13-SEP-2005 (Rel. 48, Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)

DE (Phosphopyruvate hydratase).

GN Name=ENO1;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=White leghorn; TISSUE=Kidney;

RX MEDLINE=95355305; PubMed=7629021;

RA Tanaka M., Maeda K., Nakashima K.;

RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence analysis.";

RT J. Biochem. 117:554-559 (1995).

CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.

CC -1 COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (by similarity).

CC -1 PATHWAY: Glycolysis.

CC -1 SUBUNIT: Homodimer (By similarity).

CC -1 SUBCELLULAR LOCATION: Cytoplasmic.

CC -1 SIMILARITY: Belongs to the enolase family.

CC -----

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CC -----

DR EMBL; D37900; BAA07132.1; -; mRNA.

DR PIR; JCA186; JCA186.

DR HSSP; P56252; 1PDZ.

DR SMR; P51913; 1-432.

DR Ensembl; ENSGALG0000014528; Gallus gallus.

DR InterPro; IPR000941; Enolase.

DR PANTHER; PTHR11902; Enolase; 1.

DR Pfam; PF00113; Enolase\_C; 1.

DR Pfam; PF03952; Enolase\_N; 1.

DR PRINTS; PR0148; ENOLASE.

DR ProDom; PD000902; Enolase; 1.

DR TIGRFAMs; TIGR01060; eno; 1.

DR PROSITE; PS00164; ENOLASE; 1.

KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.

FT INIT MET 0

FT ACT SITE 157

FT METAL 244

FT METAL 292

FT METAL 317

SO SEQUENCE 433 AA; 47174 MW; 93AD6B0A7AD99910 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.047;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

## RESULT 25

ENOA\_HUMAN STANDARD; PRT; 433 AA.

AC P06753; P22712; Q16704; Q658M5; Q6GMP2; Q71V37; Q723V6; Q8WU71;

AC Q9UM55;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MPB-1) (MPB-1) (Plasminogen-binding protein).

GN Name=ENO1; Synonyms=ENO1L1, MBP1, MPB1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

OC NCBI\_TaxID=9606;

OK [1]

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RX MEDLINE=86313654; PubMed=3529090;

RA Galliono A., Feo S., Moore R., Croce C.M., Showne L.C.;

RT "Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha enolase.";

RT Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745 (1986).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RX MEDLINE=90323004; PubMed=2373081;

RA Galliono A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;

RT "Structure of the human gene for alpha-enolase.";

RT Eur. J. Biochem. 190:567-573 (1990).

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORM MBP-1), AND FUNCTION.

RX MEDLINE=91172204; PubMed=2005901;

RA Ray R., Miller D.M.;

RT "Cloning and characterization of a human c-myc promoter-binding protein.";

RT Mol. Cell. Biol. 11:2154-2161 (1991).

RN [4]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE), AND MARKER FOR ENDOMETRIOSIS.

RX MEDLINE=96422099; PubMed=8824716;

RA Walter M., Leidenberger F.A., Schwepe K.W., Berg H., Northmann W.;

RT "Antireactive epitopes within the human alpha-enolase and their recognition by sera from patients with endometriosis.";

RT J. Autoimmun. 8:937-945 (1995).

RN [5]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RA Frankland J.;

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [6]

RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM ALPHA-ENOLASE).

RC TISSUE=Retina, and Stomach;

RX The German cDNA consortium;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [7]

RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM ALPHA-ENOLASE).

RC TISSUE=Brain, Eye, Lung, Ovary, Pancreatic carcinoma, and Skin;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci R.P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE OF 165-433.  
 RX MEDLINE=98317532; PubMed=963645; DOI=10.1006/geno.1997.5186;  
 RA Onyango P., Lubyova B., Gardellin P., Kurzbauer R., Welch A.,  
 RT "Molecular cloning and expression analysis of five novel genes in  
 RT chromosome 1p36.";  
 RL Genomics 50:187-198(1998).  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 170-433.  
 RC TISSUE=Brain;  
 RX MEDLINE=97264341; PubMed=9110174;  
 RA Yu W., Andersen B., Worley K.C., Muzny D.M., Ding Y., Liu W.,  
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.,  
 RT "Large-scale concatenation cDNA sequencing.";  
 RL Genome Res. 7:353-358(1997).  
 RN [10]  
 RP PROTEIN SEQUENCE OF 269-280 AND 306-320, AND INDUCTION IN DIFFUSE  
 RP LARGE CELL LYMPHOMA.  
 RX MEDLINE=95307657; PubMed=7787969;  
 RA Mohamed R.M., Hamdan M.Y., Maki A., Al-Katib A.,  
 RT "Induced expression of alpha-enolase in differentiated diffuse large  
 RT cell lymphoma.";  
 RL Enzyme Protein 48:37-44(1995).  
 RN [11]  
 RP PROTEIN SEQUENCE OF 1-8 (ISOFORM ALPHA-ENOLASE).  
 RC TISSUE=Colon carcinoma;  
 RX MEDLINE=97295306; PubMed=9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.,  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RL Electrophoresis 18:605-613(1997).  
 RN [12]  
 RP FUNCTION OF MBP1, IDENTIFICATION OF REPRESSOR DOMAINS, AND MUTAGENESIS  
 RP OF LEU-383 AND LEU-387.  
 RX MEDLINE=99182475; PubMed=10082554;  
 RA Ghosh A.K., Steele R., Ray R.B.,  
 RT "Functional domains of c-myc promoter binding protein 1 involved in  
 RT transcriptional repression and cell growth regulation.";  
 RL Mol. Cell. Biol. 19:2880-2886(1999).  
 RN [13]  
 RP FUNCTION AS A C-MYC TRANSCRIPTIONAL REPRESSOR, AND SUBCELLULAR  
 RP LOCATION.  
 RX MEDLINE=20263726; PubMed=10802057; DOI=10.1016/S0014-5793(00)01494-0;  
 RA Feo S., Arcuri D., Piddini E., Pasantino R., Gallongo A.,  
 RT "EN1 gene product binds to the c-myc promoter and acts as a  
 RT transcriptional repressor: relationship with Myc promoter-binding  
 RT protein 1 (MBP-1)."  
 RL FEBS Lett. 473:47-52(2000).  
 RN [14]  
 RP FUNCTION IN PLASMINOGEN ACTIVATION.  
 RX MEDLINE=22551878; PubMed=1266133; DOI=10.1002/ajh.10299;  
 RA Lopez-Alemay R., Longstaff C., Hawley S., Mitrani M., Fabregas P.,  
 RA Jarid M., Meron E., Miles L.A., Pelaz J.,  
 RT "Inhibition of cell surface mediated plasminogen activation by a  
 RT monoclonal antibody against alpha-enolase.";  
 RL Am. J. Hematol. 72:234-242(2003).  
 RN [15]  
 RP INTERACTION WITH PLG.  
 RX MEDLINE=97452346; PubMed=9308760;  
 RA Arza B., Pelaz J., Lopez-Alemay R., Miles L.A., Munoz-Caroves P.,  
 RT "Identification of an epitope of alpha-enolase (a candidate  
 RT plasminogen receptor) by phage display.";  
 RL Thromb. Haemost. 78:1097-1103(1997).  
 RN [16]

RP EPICTYPE MAPPING, AND ASSOCIATION WITH CAR.  
 RX MEDLINE=99096529; PubMed=9878089; DOI=10.1006/jaut.1998.0239;  
 RA Adams G., Amundson D., Seigel G.M., Machnicki M.,  
 RT "Anti-enolase-alpha autoantibodies in cancer-associated retinopathy:  
 RT epitope mapping and cytotoxicity on retinal cells.";  
 RL J. Autoimmun. 11:671-677(1998).  
 RN [17]  
 RP IDENTIFICATION OF MBP1 AS AN ALPHA ENOLASE ALTERNATIVE INITIATION  
 RP PRODUCT AND MUTAGENESIS OF MET-93 AND MET-96.  
 RX MEDLINE=20148810; PubMed=10681589; DOI=10.1074/jbc.275.8.5958;  
 RA Subramanian A., Miller D.M.,  
 RT "Structural analysis of alpha-enolase. Mapping the functional domains  
 RT involved in down-regulation of the c-myc protooncogene.";  
 RL J. Biol. Chem. 275:5958-5965(2000).  
 RN [18]  
 RP REVIEW.  
 RX MEDLINE=21388199; PubMed=11497239;  
 RA Pancholi V.,  
 RT "Multifunctional alpha-enolase: its role in diseases.";  
 RL Cell. Mol. Life Sci. 58:902-920(2001).  
 RN [19]  
 RP INTERACTION OF MBP1 WITH SBDL.  
 RX MEDLINE=20576881; PubMed=11134351; DOI=10.1128/MCB.21.2.655-662.2001;  
 RA Ghosh A.K., Majumder M., Steele R., White R.A., Ray R.B.,  
 RT "A novel 16-kilodalton cellular protein physically interacts with and  
 RT antagonizes the functional activity of c-myc promoter-binding protein  
 RT 1.";  
 RL Mol. Cell. Biol. 21:655-662(2001).  
 RN [20]  
 RP IDENTIFICATION AS AN AUTOANTIGEN IN HASHIMOTO ENCEPHALOPATHY.  
 RX MEDLINE=2223760; PubMed=12297304; DOI=10.1016/S0014-5793(02)03307-0;  
 RA Ochi H., Horinchi I., Araki N., Toda T., Araki T., Sato K., Murali H.,  
 RA Oosagawa M., Yamada T., Okamura K., Ogino T., Mizunoto K.,  
 RA Yamashita H., Sawa H., Kita J.,  
 RT "Proteomic analysis of human brain identifies alpha-enolase as a novel  
 RT autoantigen in Hashimoto's encephalopathy.";  
 RL FEBS Lett. 528:197-202(2002).  
 RN [21]  
 RP FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses. May also  
 CC function in the intravascular and pericellular fibrinolytic system  
 CC due to its ability to serve as a receptor and activator of  
 CC plasminogen on the cell surface of several cell-types such as  
 CC leukocytes and neurons.  
 CC -1- FUNCTION: MBP1 binds to the c-myc promoter and acts as a  
 CC transcriptional repressor. May be a tumor suppressor.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. EN1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/beta) form.  
 CC Query Match 72.2%; Score 65; DB 1; Length 433;  
 CC Best Local Similarity 81.2%; Pred. No. 0.047;  
 CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CC  
 CC 1 LVVGLCTCQIKTGPAC 16  
 CC ||||| |||||  
 CC 383 LVVGLCTCQIKTGPAC 398  
 CC  
 CC RESULT 26  
 CC ENOA\_MOUSE STANDARD; PRT; 433 AA.  
 CC ID\_ENOA\_MOUSE  
 CC AC P17182; Q99KT7; Q9DCV7;

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-  
 DE neutral enolase) (NNE) (Enolase 1).  
 GN Name=Eno1; Synonyms=Eno-1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RC MEDLINE=90301487; PubMed=2362815;  
 RA Kashad M., Dumont X., Chalton P., Lelias J.M., Lamande N., Lucas M.,  
 RA Lazar M., Caput D.;  
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from  
 RT mouse brain";  
 RL Nucleic Acids Res. 18:3638-3638 (1990).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Oseto N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schmitt L.M., Knapin A., Matrudu H., Batalov S., Betsel K.W.,  
 RA Blake J., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Drigani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nimata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
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 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilmink L.G., Wrynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hitotane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Ysunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 RC STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland, and Mammary tumor;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Umed T.B., Toshlyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP PROTEIN SEQUENCE OF 59-70; 99-113; 183-197 AND 245-258.  
 RC TISSUE=Macrophage;  
 RC PubMed=8427861;  
 RA Portolico L.A., Kendrick N.C., Keller A., Li Y., Tabas I.;  
 RT "Cholesteryl ester loading of mouse peritoneal macrophages is  
 RT associated with changes in the expression or modification of specific  
 RT cellular proteins, including increase in an alpha-enolase isoform";  
 RL Arterioscler. Thromb. 13:264-275 (1993).  
 RN [5]  
 RP INTERACTIONS WITH PKM2; PKM; CKM; ALDO AND TROPONIN, AND DEVELOPMENTAL  
 RP STAGE.  
 RX MEDLINE=97270626; PubMed=9169614;  
 RA Merkulova T., Lucas M., Jabet C., Lamande N., Rouzeau J.-D., Gros F.,  
 RA Lazar M., Keller A.;  
 RT "Biochemical characterization of the mouse muscle-specific enolase:  
 RT developmental changes in electrophoretic variants and selective  
 RT binding to other proteins";  
 RL Biochem. J. 323:791-800 (1997).  
 RN [6]  
 RP SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.  
 RC MEDLINE=21121273; PubMed=11229603; DOI=10.1016/S0248-4900(00)01103-5;  
 RA Keller A., Demeurille J., Merkulova T., Gerard G., Cywiler-Golzenzer C.,  
 RA Lucas M., Chatelet F.-P.;  
 RT "Fibre-type distribution and subcellular localisation of alpha and  
 RT beta enolase in mouse striated muscle";  
 RL Biol. Cell 92:527-535 (2000).  
 CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses (By similarity).  
 CC May also function in the intravascular and pericellular  
 CC fibrinolytic system due to its ability to serve as a receptor and  
 CC activator of plasminogen on the cell surface of several cell-types  
 CC such as leukocytes and neurons (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. ENO1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity). In vitro, interacts with several glycolytic enzymes  
 CC including PKM2, PKM, CKM and aldolase. Also binds troponin, in  
 CC vitro.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/gamma) form (By similarity). ENO1 is localized to the M-  
 CC band.  
 CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in  
 CC embryo and in most adult tissues. The alpha/beta heterodimer and  
 CC the beta/beta homodimer are found in striated muscle, and the  
 CC alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.  
 CC In striated muscle, expression of ENO1 appears to be independent  
 CC of fiber type.  
 CC -1- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition  
 CC from the alpha/alpha homodimer to the alpha/beta heterodimer in  
 CC striated muscle cells, and to the alpha/gamma heterodimer in nerve  
 CC cells. In embryonic muscle, ENO1 is highly expressed until E17.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.



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CC EMBL; X52379; CAA3605.1; -; mRNA.
DR EMBL; AK002336; BAB2020.1; -; mRNA.
DR EMBL; BC003891; AAH03891.1; -; mRNA.
DR EMBL; BC004017; AAH04017.1; -; mRNA.
DR EMBL; BC010685; AAH10685.1; -; mRNA.
DR EMBL; BC024644; AAH24644.1; -; mRNA.
DR EMBL; BC085098; AAH85098.1; -; mRNA.
DR PIR; S10246; S10246.
DR HSSP; P56252; 1PDZ.
DR SMR; P17182; 1-430.
DR IntAct; P17182; -.
DR SWISS-2DPAGE; P17182; MOUSE.
DR MGI; MGI:95393; Enol.
DR GO; GO:0005515; F:protein binding; TAS.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRfam; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR Direct protein sequencing; Glycolysis; Lyase; Magnesium;
KM Metal-binding; Multigene family.
FT INIT MET 0
FT REGION 404 433
FT ACT SITE 157 157
FT METAL 244 244
FT METAL 292 292
FT METAL 317 317
FT CONFLICT 358 358
SQ SEQUENCE 433 AA; 47010 MW; C90082CBA8290EB6 CRC64;

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Query Match      72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 LVVGLCTCQIKTGAPC 16
Db 383 LVVGLCTCQIKTGAPC 398

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RESULT 27
ENOA_PYTRG STANDARD; PRT; 433 AA.
AC Q9W7L0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
DE (Phosphopyruvate hydratase).
OS Python regius (Ball python) (Royal Python).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Hemophida;
OC Pythonidae; Python.
OX NCBI_TaxID=51751;
RN NM_111111;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=99439677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;
RA Mammen H., Li S.S.-L.;
RL "Molecular evidence for a clade of turtles.";
RL Mol. Phylogenet. Evol. 13:144-148(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COPACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the enolase family.

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; AF072589; AAD41646.1; -; mRNA.
DR HSSP; P56252; 1PDZ.
DR SMR; Q9W7L0; 1-432.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRfam; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.
FT INIT MET 0
FT METAL 244 244
FT METAL 292 292
FT METAL 317 317
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Query Match      72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 LVVGLCTCQIKTGAPC 16
Db 383 LVVGLCTCQIKTGAPC 398

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RESULT 28
ENOA_RAT STANDARD; PRT; 433 AA.
AC P04764; Q66H13; Q6AYY3; Q6P504;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-
DE neural enolase) (NNE) (Enolase 1).
GN Name=Enol; Synonyms=Eno-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NM_111111;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Liver;
RX MEDLINE=85242108; PubMed=2989793;
RA Sakimura K., Kushiya E., Obinata M., Takahashi Y.;
RL "Molecular cloning and the nucleotide sequence of cDNA to mRNA for
RL non-neuronal enolase (alpha alpha enolase) of rat brain and liver.";
RL Nucleic Acids Res. 13:4365-4378(1985).
RN NM_111111;
RP NUCLEOTIDE SEQUENCE.
RA Takahashi Y.;
RL Submitted (JAN-1986) to the EMBL/Genbank/DBJ databases.
RN NM_111111;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Heart, Pituitary, and Testis;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
RN NM_111111;
RP NUCLEOTIDE SEQUENCE OF 92-152.
RC TISSUE=Lymphoma;
RA Bole-Feysot C., Kelly P.A.;
RL "Rat cDNA encoding alpha enolase (2-phospho-D-glycerate hydro-lyase)
RL (non-neuronal enolase) (NNE).";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.

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RN [5]  
 RP PROTEIN SEQUENCE OF 45-56; 96-108; 244-261 AND 368-381, AND  
 RP INTERACTION WITH PLG.  
 RC TISSUE=embryonic brain;  
 RA MEDLINE=95054017; PubMed=7964722;  
 RA Nakajima K., Hamanoue M., Takemoto N., Hattori T., Kato K.,  
 RA Kohaka S.;  
 RT "Plasminogen binds specifically to alpha-enolase on rat neuronal  
 RT plasma membrane.";  
 RT J. Neurochem. 63:2048-2057(1994).  
 RN [6]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=96134716; PubMed=8594891;  
 RA Kellier A., Rouzeau J.D., Farhadian F., Wisniewsky C., Marotte F.,  
 RA Lamande N., Samuel J.L., Schwartz K., Lazar M., Lucas M.;  
 RT "Differential expression of alpha- and beta-enolase genes during rat  
 RT heart development and hypertrophy.";  
 RL Am. J. Physiol. 269:H1843-H1851(1995).  
 RN [7]  
 RP EFFECT OF THYROID HORMONES ON EXPRESSION.  
 RX MEDLINE=20131238; PubMed=10662718;  
 RA Merkulova T., Kellier A., Oliviero P., Marotte F., Samuel J.L.,  
 RA Rappaport L., Lamande N., Lucas M.;  
 RT "Thyroid hormones differentially modulate enolase isozymes during rat  
 RT skeletal and cardiac muscle development.";  
 RL Am. J. Physiol. 278:E330-E339(2000).  
 RN [8]  
 RP SUBCELLULAR LOCATION OF ALPHA/GAMMA HETERODIMER.  
 RX PubMed=15041191; DOI=10.1016/j.neures.2003.12.006;  
 RA Ueta H., Nagasawa H., Oyabu-Manabe Y., Toida K., Ishimura K., Hori H.;  
 RT "Localization of enolase in synaptic plasma membrane as an alphasgamma  
 RT heterodimer in rat brain.";  
 RL Neurosci. Res. 48:379-386(2004).  
 CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses. May also  
 CC function in the intravascular and pericellular fibrinolytic system  
 CC due to its ability to serve as a receptor and activator of  
 CC plasminogen on the cell surface of several cell-types such as  
 CC leukocytes and neurons.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COPACITOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. ENO1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/gamma) form.  
 CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in  
 CC embryo and in most adult tissues. The alpha/beta heterodimer and  
 CC the beta/beta homodimer are found in striated muscle, and the  
 CC alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.  
 CC -1- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition  
 CC from the alpha/alpha homodimer to the alpha/beta heterodimer in  
 CC striated muscle cells, and to the alpha/gamma heterodimer in nerve  
 CC cells. In brain, levels of ENO1 decrease around 10 dpc and then  
 CC gradually increase to adult age. In embryonic heart, ENO1 levels  
 CC decrease rapidly during cardiac development.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; X02610; CAA26456.1; -, mRNA.

DR EMBL; BC063174; AA63174.1; ALT INIT; mRNA.  
 DR EMBL; BC078896; AA78896.1; -, mRNA.  
 DR EMBL; BC081847; AA81847.1; ALT INIT; mRNA.  
 DR EMBL; AF241613; AA801319.1; -, mRNA.  
 DR PIR; A23126; A23126.  
 DR HSP; P56252; 1P2.  
 DR SMC; P04764; 1-430.  
 DR Ensembl; ENSRNOG00000017895; Rattus norvegicus.  
 DR RGD; 2553; Enol.  
 DR InterPro; IPR000941; Enolase.  
 DR PANTHER; PTHR11902; Enolase; 1.  
 DR Pfam; PR00113; Enolase\_C; 1.  
 DR Pfam; PF03952; Enolase\_N; 1.  
 DR PRINTS; PR0148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRFAMs; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 KW Direct protein sequencing; Glycolysis; Lyase; Magnesium;  
 KW Metal-binding; Multigene Family; Plasminogen activation.  
 FT INIT MET 0  
 FT REGION 404 433  
 FT ACT SITE 157 157  
 FT METAL 244 244  
 FT METAL 292 292  
 FT METAL 317 317  
 FT CONFLICT 47 47  
 FT CONFLICT 92 95  
 FT CONFLICT 124 124  
 FT CONFLICT 143 143  
 FT CONFLICT 150 150  
 FT CONFLICT 249 249  
 FT CONFLICT 373 373  
 SQ SEQUENCE 433 AA; 46997 MW; 61898009DACDBCC CRC64;  
 Query Match 72.2%; Score 65; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. NO. 0.047;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVNGICTGQIKTGAPC 16  
 Db 383 LVNGICTGQIKTGAPC 398  
 RESULT 29  
 ENOA\_SCEUN STANDARD; PRT; 433 AA.  
 AC Q9W7L2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)  
 DE (Phosphopyruvate hydratase).  
 OS Sceloporus undulatus (Eastern fence lizard) (Skink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylia; Squamata; Iguania; Iguanidae; Phrynosomatinae;  
 OC Sceloporus.  
 OX NCBI\_TaxID=8520;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=9943677; PubMed=10508547; DOI=10.1006/mpcv.1999.0640;  
 RA Mamen H., Li S.S.-L.;  
 RT "Molecular evidence for a clade of turtles.";  
 RL Mol. Phylogenet. Evol. 13:144-148(1999).  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COPACITOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----



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GenCore version 5.1.7  
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OM protein - protein search, using SW model

Run on: April 3, 2006, 08:03:55 ; Search time 21 Seconds  
(without alignments)  
62.991 Million cell updates/sec

Title: US-09-647-457E-3

Perfect score: 90  
Sequence: 1 LVVGLCTCQIKTGPAK 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/RTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/RB COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	72.2	434	2	US-09-949-016-6153 Sequence 6153, Ap
2	65	72.2	443	2	US-09-949-016-8359 Sequence 8359, Ap
3	46	51.1	45	1	US-07-973-852-1 Sequence 1, Appli
4	46	51.1	45	1	US-07-950-773-1 Sequence 1, Appli
5	46	51.1	46	2	US-09-030-619-230 Sequence 230, App
6	46	51.1	46	2	US-09-444-281-111 Sequence 111, App
7	45	50.0	712	2	US-09-252-991A-20471 Sequence 20471, A
8	43	47.8	100	2	US-10-105-901A-51 Sequence 51, Appl
9	43	47.8	452	2	US-09-773-877B-16 Sequence 16, Appl
10	43	47.8	462	2	US-09-773-877B-18 Sequence 18, Appl
11	43	47.8	557	2	US-09-773-877B-14 Sequence 14, Appl
12	43	47.8	567	2	US-09-773-877B-12 Sequence 12, Appl
13	43	47.8	567	2	US-09-773-877B-20 Sequence 20, Appl
14	43	47.8	661	1	US-08-232-538-12 Sequence 12, Appl
15	43	47.8	661	1	US-08-786-164-12 Sequence 12, Appl
16	43	47.8	687	1	US-08-232-538-6 Sequence 6, Appli
17	43	47.8	687	1	US-08-786-164-6 Sequence 6, Appli
18	43	47.8	687	2	US-09-427-353-2 Sequence 2, Appli
19	43	47.8	758	1	US-08-874-678-1 Sequence 1, Appli
20	43	47.8	758	1	US-08-643-839-1 Sequence 1, Appli
21	43	47.8	758	2	US-09-051-363-24 Sequence 24, Appl
22	43	47.8	758	2	US-09-348-886-1 Sequence 1, Appli
23	43	47.8	758	2	US-10-105-901A-1 Sequence 1, Appli
24	43	47.8	780	1	US-08-232-538-14 Sequence 14, Appl
25	43	47.8	780	1	US-08-786-164-14 Sequence 14, Appl
26	43	47.8	911	2	US-09-949-002-425 Sequence 425, App
27	43	47.8	1006	2	US-09-023-905A-12 Sequence 12, Appl

28	43	47.8	1006	2	US-09-949-002-361 Sequence 361, App
29	43	47.8	1311	1	US-08-340-011-5 Sequence 5, Appli
30	43	47.8	1311	2	US-08-901-710-5 Sequence 5, Appli
31	43	47.8	1311	2	US-09-169-079-5 Sequence 5, Appli
32	43	47.8	1338	2	US-08-750-141A-3 Sequence 3, Appli
33	43	47.8	1338	2	US-09-119-014D-6 Sequence 6, Appli
34	43	47.8	1362	1	US-08-874-678-33 Sequence 33, Appl
35	43	47.8	1362	2	US-08-643-839-33 Sequence 33, Appl
36	43	47.8	1362	2	US-09-348-886-33 Sequence 33, Appl
37	43	47.8	1362	2	US-10-105-901A-33 Sequence 33, Appl
38	43	47.8	3542	2	US-10-087-013-2 Sequence 2, Appli
39	42	46.7	171	2	US-09-248-796A-21129 Sequence 21129, A
40	42	46.7	444	2	US-09-252-991A-21020 Sequence 21020, A
41	42	46.7	444	2	US-09-328-352-7269 Sequence 7269, Ap
42	42	46.7	445	2	US-09-540-236-2354 Sequence 2354, Ap
43	41.5	46.1	1101	2	US-09-561-709B-5 Sequence 5, Appli
44	41.5	46.1	1342	2	US-09-561-709B-13 Sequence 13, Appl
45	41.5	46.1	1761	2	US-09-561-709B-1 Sequence 1, Appli
46	41.5	45.6	45	1	US-08-824-379-2 Sequence 2, Appli
47	41	45.6	177	1	US-08-465-794-17 Sequence 17, Appl
48	41	45.6	177	2	US-09-049-813-17 Sequence 17, Appl
49	41	45.6	177	2	US-09-227-853A-13 Sequence 13, Appl
50	41	45.6	178	1	US-08-465-794-18 Sequence 18, Appl
51	41	45.6	178	2	US-09-049-813-18 Sequence 18, Appl
52	41	45.6	178	2	US-08-663-191A-4 Sequence 4, Appli
53	40.5	45.0	2556	1	US-08-185-432-17 Sequence 17, Appl
54	40.5	45.0	2556	1	US-08-083-590A-20 Sequence 20, Appl
55	40.5	45.0	2556	2	US-08-532-384-20 Sequence 20, Appl
56	40.5	45.0	2556	2	US-08-899-232-2 Sequence 2, Appli
57	40.5	45.0	2556	2	US-09-121-457-2 Sequence 2, Appli
58	40.5	45.0	3084	2	US-09-562-702A-12 Sequence 12, Appl
59	40.5	45.0	3084	2	US-09-562-702A-10 Sequence 10, Appl
60	40	44.4	205	2	US-09-710-279-2510 Sequence 2510, Ap
61	40	44.4	300	2	US-09-198-452A-354 Sequence 354, App
62	40	44.4	341	2	US-09-438-185A-338 Sequence 338, App
63	40	44.4	476	2	US-09-252-991A-29179 Sequence 29179, A
64	40	44.4	891	2	US-09-134-001C-4913 Sequence 4913, Ap
65	40	44.4	2211	2	US-10-096-961A-1 Sequence 1, Appli
66	40	44.4	2211	2	US-10-029-217A-24 Sequence 24, Appl
67	40	44.4	3307	2	US-09-845-583A-10 Sequence 10, Appl
68	39.5	43.9	1587	2	US-09-561-709B-3 Sequence 3, Appli
69	39.5	43.9	2523	1	US-08-185-432-18 Sequence 18, Appl
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72	39.5	43.9	2523	2	US-09-177-245-273 Sequence 273, App
73	39	43.3	95	2	US-09-812-283-273 Sequence 273, App
74	39	43.3	115	2	US-09-270-767-42013 Sequence 42013, A
75	39	43.3	121	2	US-09-270-767-39953 Sequence 39953, A
76	39	43.3	121	2	US-09-270-767-55170 Sequence 55170, A
77	39	43.3	160	2	US-09-248-796A-17879 Sequence 17879, A
78	39	43.3	180	2	US-09-510-238A-286 Sequence 286, App
79	39	43.3	272	2	US-09-270-767-34757 Sequence 34757, A
80	39	43.3	272	2	US-09-270-767-49974 Sequence 49974, A
81	39	43.3	384	2	US-09-945-249-8 Sequence 8, Appli
82	39	43.3	384	2	US-09-041-990-8 Sequence 8, Appli
83	39	43.3	481	1	US-07-927-071-1 Sequence 1, Appli
84	39	43.3	481	6	5164481-1 Patent No. 5164481
85	39	43.3	689	2	US-09-177-249-2 Sequence 2, Appli
86	39	43.3	689	2	US-09-061-283-2 Sequence 2, Appli
87	39	43.3	689	2	US-09-812-283-2 Sequence 2, Appli
88	39	43.3	932	2	US-10-104-04-2128 Sequence 14, Appl
89	39	43.3	932	2	US-10-176-884-15 Sequence 15, Appl
90	39	43.3	992	1	US-08-482-847-1 Sequence 1, Appli
91	39	43.3	992	1	US-08-482-847-1 Sequence 1, Appli
92	39	43.3	1063	1	US-08-093-453B-3 Sequence 3, Appli
93	39	43.3	1063	1	US-08-127-499A-8 Sequence 8, Appli
94	39	43.3	1063	1	US-08-482-847-8 Sequence 8, Appli
95	39	43.3	1063	1	US-08-984-709A-50 Sequence 50, Appl
96	39	43.3	2353	2	US-09-086-436-30 Patent No. 5177197
97	39	43.3	2353	2	US-09-086-436-30 Patent No. 5177197
98	38.5	42.8	65	6	5177197-51 Patent No. 5177197
99	38.5	42.8	410	6	5177197-1 Patent No. 5177197
100	38.5	42.8	410	6	5177197-1 Patent No. 5177197

## ALIGNMENTS

RESULT 1  
US-09-949-016-6153; Sequence 6153, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 6153

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6153

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Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 384 LVVGLCTGQIKTGAPC 399

## RESULT 2

US-09-949-016-8359

; Sequence 8359, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 8359

; LENGTH: 443

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-8359

Query Match 72.2%; Score 65; DB 2; Length 443;  
Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 393 LVVGLCTGQIKTGAPC 408RESULT 3  
US-07-973-852-1

; Sequence 1, Application US/07973852

; Patent No. 5376640

; GENERAL INFORMATION:

; APPLICANT: Miyazaki, Toshiyuki

; APPLICANT: Motoki, Hirofumi

; APPLICANT: Kodama, Toshiaki

; APPLICANT: Maeda, Tatsuhiro

; APPLICANT: Teujita, Takahiro

; APPLICANT: Okuda, Hiromichi

; TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &amp; NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/973,852

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/631,321

; FILING DATE: 20-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 332884/1989

; FILING DATE: 25-DEC-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 75600/1990

; FILING DATE: 27-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 194782/1990

; FILING DATE: 25-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5376640man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 1327-014-0 DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 521-4500

; TELEFAX: (703) 486-2347

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-973-852-1

Query Match 51.1%; Score 46; DB 1; Length 45;  
Best Local Similarity 43.8%; Pred. No. 8.8;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 24 LCAGVCRCKISSGLSC 39

## RESULT 4

US-07-950-773-1

; Sequence 1, Application US/07950773

; Patent No. 5411956

; GENERAL INFORMATION:

; APPLICANT: Miyazaki, Toshiyuki

```

; APPLICANT: Motol, Hirofumi
; APPLICANT: Kodama, Toshiaki
; APPLICANT: Maeda, Tetsuro
; APPLICANT: Tsujita, Takahiro
; TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/950,773
; FILING DATE: 19920924
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/631,321
; FILING DATE: 20-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5411956man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1327-003-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-950-773-1

Query Match      51.1%; Score 46; DB 1; Length 45;
Best Local Similarity 43.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 LVVGLCTCQIKTGPPAC 16
Db      24 LCAGVCRCKITSSGLSC 39

RESULT 5
US-09-030-619-230
; Sequence 230, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Kriesger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Frazer, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 46
; TYPE: PRT

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; ORGANISM: Hordeum vulgare
US-09-030-619-230

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Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GLCTCQIKTGPPAC 16
Db      28 GACRCCKITSSGPC 40

RESULT 6
US-09-444-281-111
; Sequence 111, Application US/09444281
; Patent No. 6946261
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/09/444,281
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-444-281-111

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Query Match      51.1%; Score 46; DB 2; Length 46;
Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GLCTCQIKTGPPAC 16
Db      28 GACRCCKITSSGPC 40

```

```

RESULT 7
US-09-252-991A-20471
; Sequence 20471, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.156
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20471
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20471

Query Match      50.0%; Score 45; DB 2; Length 712;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy      2 VVGLCTCQIKTGPPAC 16
Db      641 VTGSCRCNASSPPAC 655

RESULT 8

```

US-10-105-901A-51  
; Sequence 51, Application US/10105901A  
; Patent No. 6897294  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; Chen, Helen H.  
; Presta, Leonard  
; Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
; GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
; PRODUCTION  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dorsney & Whitney LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/105,901A  
; FILING DATE: 20-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/348,886  
; FILING DATE: 01-JUL-1999  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard F. Treacartin  
; REGISTRATION NUMBER: 31,801  
; REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-10-105-901A-51  
  
Query Match 47.8%; Score 43; DB 2; Length 100;  
Best Local Similarity 50.0%; Pred. No. 47;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 GLCTCQIKTGA 15  
DB 76 GLYTCRVRSGPS 87  
  
RESULT 9  
US-09-773-877B-16  
; Sequence 16, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 16

; LENGTH: 452  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1(2-3 deltab)-Fc  
US-09-773-877B-16  
  
Query Match 47.8%; Score 43; DB 2; Length 452;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 GLCTCQIKTGA 15  
DB 192 GLYTCRVRSGPS 203  
  
RESULT 10  
US-09-773-877B-18  
; Sequence 18, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 18  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1(2-3)-Fc (Muc3)  
US-09-773-877B-18  
  
Query Match 47.8%; Score 43; DB 2; Length 462;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 GLCTCQIKTGA 15  
DB 202 GLYTCRVRSGPS 213  
  
RESULT 11  
US-09-773-877B-14  
; Sequence 14, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 14  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1(1-3 deltab)-Fc (Muc1)  
US-09-773-877B-14  
  
Query Match 47.8%; Score 43; DB 2; Length 557;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 GLCTCQIKTGA 15  
DB 297 GLYTCRVRSGPS 308



RESULT 12  
US-09-773-877B-12  
Sequence 12, Application US/09773877B  
Patent No. 6833349  
GENERAL INFORMATION:  
APPLICANT: Xia, Yu-Ping et al.  
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
FILE REFERENCE: REG 710B  
CURRENT APPLICATION NUMBER: US/09/773,877B  
CURRENT FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 12  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flc(1-3)-Fc  
US-09-773-877B-12

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GLCTCOIKTGPA 15  
Db 307 GLYTCRVSGPS 318

RESULT 13  
US-09-773-877B-20  
Sequence 20, Application US/09773877B  
Patent No. 6833349  
GENERAL INFORMATION:  
APPLICANT: Xia, Yu-Ping et al.  
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
FILE REFERENCE: REG 710B  
CURRENT APPLICATION NUMBER: US/09/773,877B  
CURRENT FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 20  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flc(1-3 R-N)-Fc (Mut4)  
US-09-773-877B-20

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GLCTCOIKTGPA 15  
Db 307 GLYTCRVSGPS 318

RESULT 14  
US-08-233-538-12  
Sequence 12, Application US/08232538  
Patent No. 5712380  
GENERAL INFORMATION:  
APPLICANT: Thomas, Kenneth A.  
APPLICANT: Kendall, Richard L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000 126 E Lincoln Avenue  
CITY: Rahway

STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,538  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mallen, John W. III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 188881A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 661 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-232-538-12

Query Match 47.8%; Score 43; DB 1; Length 661;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GLCTCOIKTGPA 15  
Db 281 GLYTCRVSGPS 292

RESULT 15  
US-08-786-164-12  
Sequence 12, Application US/08786164  
Patent No. 5861484  
GENERAL INFORMATION:  
APPLICANT: THOMAS, KENNETH A.  
APPLICANT: KENDALL, RICHARD L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: CELL GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/786,164  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Hard, J  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18888DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720

```
TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 661 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-786-164-12

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 661;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 281 GLYTCRVRSGPS 292

RESULT 16
US-08-232-538-6
; Sequence 6, Application US/08232538
; Patent No. 5712380
; GENERAL INFORMATION:
;   APPLICANT: Thomas, Kenneth A.
;   APPLICANT: Kendall, Richard L.
;   TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
;   NUMBER OF INVENTIONS: GROWTH FACTOR
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merck & Co., Inc.
;   STREET: P.O. Box 2000 126 E Lincoln Avenue
;   CITY: Rahway
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,538
;   FILING DATE:
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wallen, John W.III
;   REGISTRATION NUMBER: 35,403
;   REFERENCE/DOCKET NUMBER: 188881A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (908) 594-3905
;   TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 687 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-232-538-6

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 687;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 17
US-08-786-164-6
; Sequence 6, Application US/08786164
```

```
Patent No. 5861484
; GENERAL INFORMATION:
;   APPLICANT: THOMAS, KENNETH A.
;   APPLICANT: KENDALL, RICHARD L.
;   TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
;   NUMBER OF INVENTIONS: CELL GROWTH FACTOR
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merck & Co., Inc.
;   STREET: P.O. Box 2000, 126 E. Lincoln Ave.
;   CITY: Rahway
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/786,164
;   FILING DATE: 21-JAN-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mark Hand, J
;   REGISTRATION NUMBER: 36,545
;   REFERENCE/DOCKET NUMBER: 18888DA
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 908-594-3905
;   TELEFAX: 908-594-4720
;   TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 687 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-786-164-6

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 687;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 18
US-09-427-353-2
; Sequence 2, Application US/09427353
; Patent No. 6375929
; GENERAL INFORMATION:
;   APPLICANT: THOMAS, KENNETH A.
;   APPLICANT: GOLDMAN, COREY K.
;   APPLICANT: KENDALL, RICHARD L.
;   APPLICANT: BETT, ANDREW J.
;   TITLE OF INVENTION: HUCKLE, WILLIAM R.
;   TITLE OF INVENTION: GENE THERAPY FOR INHIBITION OF
;   NUMBER OF INVENTIONS: ANGIOGENESIS
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
;   STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
;   CITY: RAHWAY
;   STATE: NJ
;   COUNTRY: US
;   ZIP: 07065-0907
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/427,353  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19810YCA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-09-427-353-2

Query Match 47.8%; Score 43; DB 2; Length 687;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKTGA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 19  
US-08-874-678-1  
Sequence 1, Application US/08874678  
Patent No. 5952199  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/874,678  
FILING DATE: HERWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Dregger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63291-1/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-874-678-1

Query Match 47.8%; Score 43; DB 1; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKTGA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 20  
US-08-643-839-1  
Sequence 1, Application US/08643839  
Patent No. 6100071  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,839  
FILING DATE: 07-MAY-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63291/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-643-839-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
|||:||||:  
Db 307 GLYTCRVRSGPS 318

RESULT 21  
US-09-051-363-24  
; Sequence 24, Application US/09051363  
; Patent No. 6270993  
; GENERAL INFORMATION:  
; APPLICANT: Shibuya, Masabumi  
; APPLICANT: Okamoto, Masaaji  
; APPLICANT: Niwa, Mikio  
; APPLICANT: Matsumoto, Tomoe  
; APPLICANT: Asano, Makoto  
; APPLICANT: Segawa, Toshiaki  
; TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/051,363  
; FILING DATE: 07-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP96/02906  
; FILING DATE: 07-OCT-1996  
; APPLICATION NUMBER: 8/211892 JP  
; FILING DATE: 23-JUL-1996  
; APPLICATION NUMBER: 7/296476 JP  
; FILING DATE: 07-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Ph.D., J.D., Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 06501/012001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-051-363-24

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
|||:||||:  
Db 307 GLYTCRVRSGPS 318

RESULT 22  
US-09-348-886-1  
; Sequence 1, Application US/09348886  
; Patent No. 6383486  
; GENERAL INFORMATION:

; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/348,886  
; FILING DATE: 01-JUL-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dolly A. Vance  
; REGISTRATION NUMBER: 39,054  
; REFERENCE/DOCKET NUMBER: A-63291-2/RMS/DAV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-09-348-886-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
|||:||||:  
Db 307 GLYTCRVRSGPS 318

RESULT 23  
US-10-105-901A-1  
; Sequence 1, Application US/10105901A  
; Patent No. 6897294  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dorsey & Whitney LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/105,901A  
FILING DATE: 20-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/348,886  
FILING DATE: 01-JUL-1999  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard F. Treccatlin  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-105-901A-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 24  
US-08-232-538-14  
Sequence 14, Application US/08232538  
Patent No. 5712380  
GENERAL INFORMATION:  
APPLICANT: Thomas, Kenneth A.  
APPLICANT: Kendall, Richard L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000 126 E Lincoln Avenue  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,538  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W.III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 188881A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-232-538-14

Query Match 47.8%; Score 43; DB 1; Length 780;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 25  
US-08-786-164-14  
Sequence 14, Application US/08786164  
Patent No. 5861484  
GENERAL INFORMATION:  
APPLICANT: THOMAS, KENNETH A.  
APPLICANT: KENDALL, RICHARD L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: CELL GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/786,164  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Hard, J  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18888DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-786-164-14

Query Match 47.8%; Score 43; DB 1; Length 780;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
DB 307 GLYTCRVRSGPS 318

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RESULT 26
US-09-949-002-425
; Sequence 425, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-425

Query Match          47.8%; Score 43; DB 2; Length 911;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 VGLCTCQIKTGP 14
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Db      365 LNLITCQVKTNP 376

RESULT 27
US-09-023-905A-12
; Sequence 12, Application US/09023905A
; Patent No. 6475778
; GENERAL INFORMATION:
; APPLICANT: Roberts, Thomas M.
; APPLICANT: King, Frederick J.
; APPLICANT: Harris, David F.
; APPLICANT: Hu, Erding
; APPLICANT: Spiegelman, Bruce
; APPLICANT: Chan, Joanne
; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: DFN-021
; CURRENT APPLICATION NUMBER: US/09/023,905A
; CURRENT FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/038,191
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-023-905A-12

Query Match          47.8%; Score 43; DB 2; Length 1006;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 VGLCTCQIKTGP 14
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Db      349 LNLITCQVKTNP 360

RESULT 28
US-09-949-002-361
; Sequence 361, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-361

Query Match          47.8%; Score 43; DB 2; Length 1006;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 VGLCTCQIKTGP 14
       : |||||
Db      349 LNLITCQVKTNP 360

RESULT 29
US-08-340-011-5
; Sequence 5, Application US/08340011
; Patent No. 5776755
; GENERAL INFORMATION:
; APPLICANT: Altalo, et al.
; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,011
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959,951
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 32267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-011-5

Query Match          47.8%; Score 43; DB 1; Length 1311;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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OY 4 GLCTCQIKTGPA 15  
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 DB 317 GLYTCRVRSGPS 328

RESULT 30

US-08-901-710-5  
 / Sequence 5, Application US/08901710  
 / Patent No. 6107046  
 / GENERAL INFORMATION:  
 / APPLICANT: Alitalo, Kari  
 / APPLICANT: Apellikova, Olga  
 / APPLICANT: Pajusola, Katri  
 / APPLICANT: Armstrong, Elna  
 / APPLICANT: Korhonen, Jaana  
 / APPLICANT: Kaipainen, Arja  
 / APPLICANT: Mälikäinen, Marja-Terttu  
 / TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES  
 / TITLE OF INVENTION: THEREOF  
 / NUMBER OF SEQUENCES: 20  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 / STREET: 6300 Sears Tower, 233 South Wacker Drive  
 / CITY: Chicago  
 / STATE: Illinois  
 / COUNTRY: United States of America  
 / ZIP: 60606-6402  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patentin Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/901,710  
 / FILING DATE:  
 / CLASSIFICATION: 435  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/340,011  
 / FILING DATE: 14-NOV-1994  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/257,754  
 / FILING DATE: 09-JUL-1994  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 07/959,951  
 / FILING DATE: 09-OCT-1992  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Gass, David A.  
 / REGISTRATION NUMBER: 38,153  
 / REFERENCE/DOCKET NUMBER: 28113/33824  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 312/474-6300  
 / TELEFAX: 312/474-0448  
 / TELEX: 25-3856  
 / INFORMATION FOR SEQ ID NO: 5:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 1311 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: peptide  
 / US-08-901-710-5

Query Match 47.8%; Score 43; DB 2; Length 1311;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGPA 15  
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 DB 317 GLYTCRVRSGPS 328

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 Job time : 23 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:04:51 ; Search time 166 Seconds  
(without alignments)  
40.273 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVWGLTCQIKTGAPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_AA\_Main:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	5	US-10-733-969A-13 Sequence 13, Appl
2	74	82.2	458	5	US-10-478-519-6 Sequence 6, Appl
3	65	72.2	50	5	US-10-776-013-325 Sequence 325, App
4	65	72.2	269	5	US-10-473-127-1043 Sequence 1043, Ap
5	65	72.2	272	5	US-10-473-127-1041 Sequence 1041, Ap
6	65	72.2	272	5	US-10-473-127-1041 Sequence 1041, Ap
7	65	72.2	336	5	US-10-473-127-1042 Sequence 1042, Ap
8	65	72.2	420	5	US-10-498-788-17 Sequence 17, Appl
9	65	72.2	429	5	US-10-473-127-604 Sequence 604, App
10	65	72.2	433	3	US-09-935-642-9 Sequence 9, Appl
11	65	72.2	433	5	US-10-733-969A-61 Sequence 61, Appl
12	65	72.2	433	5	US-10-473-127-608 Sequence 608, App
13	65	72.2	433	5	US-10-473-127-610 Sequence 610, App
14	65	72.2	434	4	US-10-177-293-124 Sequence 124, App
15	65	72.2	434	4	US-10-205-194-47 Sequence 47, Appl
16	65	72.2	434	4	US-10-354-358-16 Sequence 16, Appl
17	65	72.2	434	4	US-10-170-385-257 Sequence 257, App
18	65	72.2	434	4	US-10-170-385-273 Sequence 273, App
19	65	72.2	434	4	US-10-258-666-10 Sequence 10, Appl
20	65	72.2	434	4	US-10-205-331-26 Sequence 26, Appl
21	65	72.2	434	5	US-10-473-127-595 Sequence 595, App
22	65	72.2	434	5	US-10-473-127-596 Sequence 596, App
23	65	72.2	434	5	US-10-473-127-597 Sequence 597, App
24	65	72.2	434	5	US-10-473-127-598 Sequence 598, App
25	65	72.2	434	5	US-10-473-127-599 Sequence 599, App
26	65	72.2	434	5	US-10-473-127-600 Sequence 600, App
27	65	72.2	434	5	US-10-473-127-601 Sequence 601, App

28	65	72.2	434	5	US-10-473-127-602 Sequence 602, App
29	65	72.2	434	5	US-10-473-127-603 Sequence 603, App
30	65	72.2	434	5	US-10-473-127-609 Sequence 609, App
31	65	72.2	434	5	US-10-723-860-1117 Sequence 1717, Ap
32	65	72.2	434	5	US-10-723-860-1948 Sequence 1948, Ap
33	65	72.2	434	5	US-10-370-715B-38 Sequence 38, Appl
34	65	72.2	434	5	US-10-873-595-15 Sequence 15, Appl
35	65	72.2	434	5	US-10-489-740-146 Sequence 146, Appl
36	65	72.2	434	5	US-10-491-548A-36 Sequence 36, Appl
37	65	72.2	434	5	US-10-676-691-13 Sequence 13, Appl
38	65	72.2	434	5	US-10-676-691-15 Sequence 15, Appl
39	65	72.2	434	5	US-10-676-691-21 Sequence 21, Appl
40	65	72.2	434	5	US-10-676-691-22 Sequence 22, Appl
41	65	72.2	434	5	US-10-676-691-23 Sequence 23, Appl
42	65	72.2	434	5	US-10-287-436A-373 Sequence 373, App
43	65	72.2	434	5	US-10-287-436A-1074 Sequence 1074, Ap
44	65	72.2	434	5	US-10-676-691-24 Sequence 24, Appl
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46	65	72.2	434	5	US-10-676-691-22 Sequence 22, Appl
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50	52	57.8	200	4	US-10-437-963-182579 Sequence 182579, A
51	52	57.8	372	4	US-10-437-963-192575 Sequence 192575, A
52	51	56.7	66	3	US-09-864-408A-6276 Sequence 6276, Ap
53	51	56.7	103	4	US-10-437-963-192583 Sequence 192583, A
54	51	56.7	211	4	US-10-425-114-57843 Sequence 57843, A
55	51	56.7	245	4	US-10-425-114-46733 Sequence 46733, A
56	51	56.7	292	4	US-10-437-963-144071 Sequence 144071, A
57	51	56.7	447	4	US-10-425-115-212253 Sequence 212253, A
58	50	55.6	90	4	US-10-425-115-264306 Sequence 264306, A
59	50	55.6	152	4	US-10-425-114-48757 Sequence 48757, A
60	50	55.6	226	4	US-10-425-114-56560 Sequence 56560, A
61	50	55.6	284	4	US-10-425-114-43844 Sequence 43844, A
62	50	55.6	286	4	US-10-424-559-156709 Sequence 156709, A
63	50	55.6	287	4	US-10-424-559-156701 Sequence 156701, A
64	50	55.6	411	4	US-10-767-701-47263 Sequence 47263, A
65	50	55.6	444	4	US-10-425-115-261716 Sequence 261716, A
66	50	55.6	447	4	US-10-424-559-261184 Sequence 261184, A
67	50	55.6	447	4	US-10-369-493-3639 Sequence 3639, Ap
68	49	54.4	164	4	US-10-425-114-64646 Sequence 64646, A
69	49	54.4	177	4	US-10-425-114-46609 Sequence 46609, A
70	49	54.4	220	4	US-10-425-114-51600 Sequence 51600, A
71	49	54.4	260	4	US-10-425-114-68956 Sequence 68956, A
72	49	54.4	284	4	US-10-425-115-258706 Sequence 258706, A
73	49	54.4	94	4	US-10-425-114-45521 Sequence 45521, A
74	48	53.3	110	4	US-10-425-115-207365 Sequence 207365, A
75	48	53.3	113	4	US-10-767-701-57224 Sequence 57224, A
76	48	53.3	201	4	US-10-425-114-43256 Sequence 43256, A
77	48	53.3	403	4	US-10-437-963-111671 Sequence 111671, A
78	48	53.3	476	5	US-10-739-930-8212 Sequence 8212, Ap
79	48	53.3	512	4	US-10-425-114-43444 Sequence 43444, A
80	48	53.3	529	4	US-10-425-115-207367 Sequence 207367, A
81	48	53.3	2037	4	US-10-184-664-591 Sequence 591, App
82	48	53.3	2037	4	US-10-184-664-591 Sequence 591, App
83	48	53.3	2542	4	US-10-123-155-95 Sequence 95, Appl
84	48	53.3	2542	4	US-10-146-721-95 Sequence 95, Appl
85	48	53.3	2542	4	US-10-146-721-95 Sequence 95, Appl
86	48	53.3	2542	4	US-10-146-721-95 Sequence 95, Appl
87	48	53.3	2542	4	US-10-141-761-95 Sequence 95, Appl
88	48	53.3	2542	4	US-10-141-761-95 Sequence 95, Appl
89	48	53.3	2542	4	US-10-142-885-95 Sequence 95, Appl
90	48	53.3	2542	4	US-10-158-790-95 Sequence 95, Appl
91	48	53.3	2542	4	US-10-137-871-95 Sequence 95, Appl
92	48	53.3	2542	4	US-10-140-923-95 Sequence 95, Appl
93	48	53.3	2542	4	US-10-141-756-95 Sequence 95, Appl
94	48	53.3	2542	4	US-10-141-759-95 Sequence 95, Appl
95	48	53.3	2542	4	US-10-140-805-95 Sequence 95, Appl
96	48	53.3	2542	4	US-10-140-805-95 Sequence 95, Appl
97	48	53.3	4277	4	US-10-184-644-439 Sequence 439, App
98	47	52.2	59	4	US-10-184-644-439 Sequence 439, App
99	47	52.2	166	4	US-10-424-559-173064 Sequence 173064, A
100	46.5	51.7	437	4	US-10-425-115-259324 Sequence 259324, A

## ALIGNMENTS

RESULT 1

```
US-10-733-969A-13
; Sequence 13, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733, 969A
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 02028058.2
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Alpha enolase; Accession NO: as of 06 Dec 2002: Q05524
US-10-733-969A-13
```

```
Query Match      82.2%; Score 74; DB 5; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.023;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGPAC 16

Db 407 LVVGLCTGQIKTGPTC 422

## RESULT 2

```
US-10-478-519-6
; Sequence 6, Application US/10478519
; Publication No. US20050042738A1
; GENERAL INFORMATION:
; APPLICANT: SMARNAKAR, Anita; GORVAD, Ann E.;
; APPLICANT: HAPALIA, April J.A.; DUGGAN, Brendan M.;
; APPLICANT: EMERLING, Brooke M.; ISON, Craig H.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; YUE, HuiBin;
; APPLICANT: FORSYTHE, Ian J.; LI, Joana X.;
; APPLICANT: THANGAVELU, Kavitha; CHAMULA, Narinder K.;
; APPLICANT: BURFORD, Neil; MASON, Patricia M.;
; APPLICANT: LAL, Preeti G.; LEE, Sally;
; APPLICANT: BECHA, Shanya D.; TANG, Y. Tom
; TITLE OF INVENTION: Carbohydrate-Associated Proteins
; FILE REFERENCE: EP-0982 USN
; CURRENT APPLICATION NUMBER: US/10/478, 519
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/18354
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293, 768
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/309, 548
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/314, 400
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 60/343, 706
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/337, 999
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
```

```
; SEQ ID NO 6
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7488348CD1
US-10-478-519-6
```

```
Query Match      82.2%; Score 74; DB 5; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.023;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGPAC 16

Db 407 LVVGLCTGQIKTGPTC 422

## RESULT 3

```
US-10-776-013-325
; Sequence 325, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: ROCH, Jean-Marc
; APPLICANT: BARTEL, Paul
; APPLICANT: HEICHMAN, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776, 013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-325
```

```
Query Match      72.2%; Score 65; DB 5; Length 50;
Best Local Similarity 81.2%; Pred. No. 0.058;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGPAC 16

Db 24 LVVGLCTGQIKTGAPC 39

## RESULT 4

```
US-10-473-127-1043
; Sequence 1043, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOB Inc.
```

```

; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1043
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1043
```

```
Query Match          72.2%; Score 65; DB 5; Length 269;
Best Local Similarity 81.2%; Pred. No. 0.26;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGQIKTGAPC 16
Db      219 LVVGLCTGQIKTGAPC 234
```

```

RESULT 5
US-10-473-127-1041
; Sequence 1041, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1041
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1041
```

```
Query Match          72.2%; Score 65; DB 5; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGQIKTGAPC 16
Db      222 LVVGLCTGQIKTGAPC 237
```

RESULT 6

```

US-10-473-127-1044
; Sequence 1044, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1044
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1044
```

```
Query Match          72.2%; Score 65; DB 5; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGQIKTGAPC 16
Db      222 LVVGLCTGQIKTGAPC 237
```

```

RESULT 7
US-10-473-127-1042
; Sequence 1042, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1042
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1042
```

```
Query Match          72.2%; Score 65; DB 5; Length 336;
Best Local Similarity 81.2%; Pred. No. 0.32;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 LVVGLCTGQIKTGAPC 16
```

Db 286 LVVGLCTGQIKTGAPC 301

RESULT 8

US-10-498-788-17  
; Sequence 17, Application US/10498788  
; Publication No. US20050118594A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: Chawla, Narinder K.  
; APPLICANT: Lee, Soo Yeun  
; APPLICANT: Ring, Huijun Z.  
; APPLICANT: Lee, Ernestine A.  
; APPLICANT: Forsythe, Ian J.  
; APPLICANT: Khare, Reena  
; APPLICANT: Tran, Uyen K.  
; APPLICANT: Kable, Amy E.  
; APPLICANT: Richardson, Thomas W.  
; APPLICANT: Emerling, Brooke M.  
; APPLICANT: Lindquist, Erika A.  
; APPLICANT: Baughn, Mariah R.  
; APPLICANT: Hafalia, April J. A.  
; APPLICANT: Jin, Pei  
; APPLICANT: Swarnakar, Anita  
; APPLICANT: Li, Joana X.  
; APPLICANT: Marquis, Joseph P.  
; APPLICANT: Lee, Sally  
; APPLICANT: Gorvad, Ann E.  
; APPLICANT: Sprague, William W.  
; APPLICANT: Bedna, Shanya D.  
; APPLICANT: Elliott, Vicki S.  
; TITLE OF INVENTION: ENZYMES  
; FILE REFERENCE: PF-1312 PCT  
; CURRENT APPLICATION NUMBER: US/10498,788  
; CURRENT FILING DATE: 2004-06-14  
; PRIOR APPLICATION NUMBER: US 60/340,357  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/342,962  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/343,558  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/351,107  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PERL Program  
; SEQ ID NO 17  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7506054CD1  
US-10-498-788-17

Query Match 72.2%; Score 65; DB 5; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.39;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 370 LVVGLCTGQIKTGAPC 385

RESULT 9

US-10-473-127-604  
; Sequence 604, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10473,127

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/279,495

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310,801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336,780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358,985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 604

; LENGTH: 429

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-473-127-604

Query Match 72.2%; Score 65; DB 5; Length 429;

Best Local Similarity 81.2%; Pred. No. 0.4;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 379 LVVGLCTGQIKTGAPC 394

RESULT 10

US-09-935-642-9  
; Sequence 9, Application US/09935642  
; Publication No. US20030044795A1  
; GENERAL INFORMATION:  
; APPLICANT: BYRJALSEN, Inger  
; APPLICANT: LARSEN, Peter  
; APPLICANT: STEPHEN, John  
; TITLE OF INVENTION: Biochemical Markers for the Human  
; FILE REFERENCE: 8969-014  
; CURRENT APPLICATION NUMBER: US/09935,642  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: PCT/GB97/02394  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2  
; PRIOR FILING DATE: 1996-09-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 433  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-642-9

Query Match 72.2%; Score 65; DB 3; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 11

US-10-733-969A-61  
; Sequence 61, Application US/10733969A  
; Publication No. US20040219572A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, JIE  
; APPLICANT: HU, LIPING

APPLICANT: LIU, TONG HUA  
APPLICANT: LU, ZHAO HUI  
APPLICANT: SHEN, YAN  
TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER  
FILE REFERENCE: 21525  
CURRENT APPLICATION NUMBER: US/10/733,969A  
CURRENT FILING DATE: 2003-12-11  
PRIOR APPLICATION NUMBER: EP 02028058.2  
PRIOR FILING DATE: 2002-12-17  
NUMBER OF SEQ ID NOS: 110  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 61  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha enolase; Accession NO:  
OTHER INFORMATION: as of 29 August 2003; P06733  
US-10-733-969A-61

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 12  
US-10-473-127-608  
Sequence 608, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 608  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-608

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 13  
US-10-473-127-610  
Sequence 610, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:

APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 610  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-610

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 14  
US-10-177-293-124  
Sequence 124, Application US/10177293  
Publication No. US20030124128A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Glatc, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Ganavarpur Manjula  
APPLICANT: Kamakkar, Shubhangi  
APPLICANT: Mertens, Maureen  
APPLICANT: Myer, Ylic  
APPLICANT: Wang, Youzhen  
APPLICANT: Xu, Yongyao  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Monahan, John  
APPLICANT: Meyers, Rachel E.  
APPLICANT: Baat Jr., Robert C.  
APPLICANT: Horobagyl, Gabriel N.  
APPLICANT: Pusztai, Lajos  
APPLICANT: Meric, Funda  
APPLICANT: Sahin, Aysegul  
APPLICANT: Mills, Gordon B.  
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
FILE REFERENCE: MRI-038  
CURRENT APPLICATION NUMBER: US/10/177,293  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 60/299,887  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301,572  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/306,501  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/325,002  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/362,585  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/xxx,xxx

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; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-124

Query Match      72.2%  Score 65; DB 4; Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
DB      384 LVVGLCTGQIKTGAPC 399

RESULT 15
US-10-205-194-47
; Sequence 47, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alstair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Plincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WI-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; PRIOR FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Neuron-specific enolase
US-10-205-194-47

Query Match      72.2%  Score 65; DB 4; Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
DB      384 LVVGLCTGQIKTGAPC 399

RESULT 16
US-10-354-358-16
; Sequence 16, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Teal, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamsen, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2039,
```

```

; TITLE OF INVENTION: 2150, 26593, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P/RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-16

Query Match      72.2%  Score 65; DB 4; Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
DB      384 LVVGLCTGQIKTGAPC 399

RESULT 17
US-10-170-385-257
; Sequence 257, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-385-257
```

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 18  
US-10-170-385-273  
Sequence 273, Application US/10170385  
Publication No. US20030203372A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Neil Raymond  
APPLICANT: Mundy, Christopher Robert  
APPLICANT: Kan, On  
APPLICANT: Harris, Robert Alan  
APPLICANT: White, Jonathan  
APPLICANT: Binley, Katie Mary  
APPLICANT: Rayner, William Nigel  
APPLICANT: Naylor, Stuart  
APPLICANT: Kingsman, Susan Mary  
APPLICANT: Krige, David  
TITLE OF INVENTION: ANALYSIS METHOD  
FILE REFERENCE: 532682000100  
CURRENT APPLICATION NUMBER: US/10/170,385  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: PCT/GB02/01662  
PRIOR FILING DATE: 2002-04-08  
PRIOR APPLICATION NUMBER: PCT/GB01/05458  
PRIOR FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 549  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 273  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-170-385-273

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 19  
US-10-258-666-10  
Sequence 10, Application US/10258666  
Publication No. US20040005578A1  
GENERAL INFORMATION:  
APPLICANT: Yamada, Yoji  
APPLICANT: Sekine, Susumu  
APPLICANT: Kikuchi, Yasuhiro  
APPLICANT: Sakurada, Kazuhito  
APPLICANT: Kyowa Hako Kogyo Co., Ltd.  
TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes  
FILE REFERENCE: 082382-000000US  
CURRENT APPLICATION NUMBER: US/10/258,666  
CURRENT FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: JP 2000-126741  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: WO PCT/JP01/03700  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Rattus norvegicus

FEATURE:  
OTHER INFORMATION: RHDH-099, non-neuronal enolase  
US-10-258-666-10

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 20  
US-10-205-331-26  
Sequence 26, Application US/10205331  
Publication No. US20040058326A1  
GENERAL INFORMATION:  
APPLICANT: Warner-Lambert Company  
APPLICANT: Lee, Kevin  
APPLICANT: Dixon, Alister  
APPLICANT: Brooksbank, Robert  
APPLICANT: Pincock, Robert  
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
FILE REFERENCE: WL-A-018199  
CURRENT APPLICATION NUMBER: US/10/205,331  
CURRENT FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: GB 0118354.0  
PRIOR FILING DATE: 2001-07-27  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Alpha-enolase  
US-10-205-331-26

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 21  
US-10-473-127-595  
Sequence 595, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 595

```
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-595
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 22
US-10-473-127-596
; Sequence 596, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-596
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 23
US-10-473-127-597
; Sequence 597, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
```

```
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-597
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 24
US-10-473-127-598
; Sequence 598, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 598
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-598
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 25
US-10-473-127-599
; Sequence 599, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
```



```
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 599
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-599
```

```
Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 26
US-10-473-127-600
; Sequence 600, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 600
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-600
```

```
Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 27
US-10-473-127-601
; Sequence 601, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
```

```
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 601
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-601
```

```
Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 28
US-10-473-127-602
; Sequence 602, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 602
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-602
```

```
Query Match 72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 29
US-10-473-127-603
; Sequence 603, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
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Search completed: April 3, 2006, 08:17:02  
Job time : 168 secs

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; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 603
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-603

```

```

Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399

```

```

RESULT 30
US-10-473-127-609
; Sequence 609, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 609
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-609

```

```

Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399

```

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: Apr11 3, 2006, 08:07:10 ; Search time 12 Seconds  
(without alignments)  
40.589 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVWGLCTCQIKTGPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA New:\*  
1: /SIDS/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
2: /SIDS/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /SIDS/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
4: /SIDS/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
5: /SIDS/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
6: /SIDS/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
7: /SIDS/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
8: /SIDS/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	82.2	458	6	US-10-878-556A-28 Sequence 28, Appl
2	65	72.2	434	6	US-10-821-234-1553 Sequence 1553, Ap
3	65	72.2	434	7	US-11-168-637-10 Sequence 10, Appl
4	47.5	52.8	1620	6	US-10-055-877-213 Sequence 213, App
5	47.5	52.8	1664	6	US-10-055-877-212 Sequence 212, App
6	46	51.1	46	7	US-11-068-783-111 Sequence 111, App
7	45.5	50.6	127	7	US-11-172-740-2156 Sequence 2156, Ap
8	43	47.8	100	7	US-11-043-693-51 Sequence 51, Appl
9	43	47.8	452	7	US-11-016-503-6 Sequence 6, Appl
10	43	47.8	462	7	US-11-016-503-8 Sequence 8, Appl
11	43	47.8	557	7	US-11-016-503-4 Sequence 4, Appl
12	43	47.8	567	7	US-11-016-503-2 Sequence 2, Appl
13	43	47.8	567	7	US-11-016-503-10 Sequence 10, Appl
14	43	47.8	758	7	US-11-043-693-11 Sequence 11, Appl
15	43	47.8	1338	6	US-10-821-234-1622 Sequence 1622, Ap
16	43	47.8	1338	7	US-11-109-156-23 Sequence 23, Appl
17	43	47.8	1338	7	US-11-075-047A-2 Sequence 2, Appl
18	43	47.8	1362	7	US-11-043-693-33 Sequence 33, Appl
19	42	46.7	296	7	US-11-182-343-31 Sequence 31, Appl
20	42	46.7	360	7	US-11-112-240-1 Sequence 1, Appl
21	42	46.7	360	7	US-11-112-304A-1 Sequence 1, Appl
22	42	46.7	544	6	US-10-980-388-40 Sequence 40, Appl
23	41	45.6	839	7	US-11-096-568A-24462 Sequence 24462, A
24	41	45.6	878	7	US-11-096-568A-24461 Sequence 24461, A
25	41	45.6	909	7	US-11-096-568A-24460 Sequence 24460, A

26	40.5	45.0	1433	7	US-11-114-962-1 Sequence 1, Appl
27	40.5	45.0	2556	7	US-11-050-346-67 Sequence 67, Appl
28	40	44.4	205	6	US-10-793-626-2510 Sequence 2510, Ap
29	39.5	43.9	1356	6	US-10-894-592-3 Sequence 3, Appl
30	39.5	43.9	257	7	US-11-096-051-12 Sequence 12, Appl
31	39.5	43.9	296	7	US-11-096-051-18 Sequence 18, Appl
32	39.5	43.9	821	7	US-11-096-051-6 Sequence 6, Appl
33	39.5	43.9	862	7	US-11-096-051-20 Sequence 20, Appl
34	39.5	43.9	2376	7	US-11-096-051-4 Sequence 4, Appl
35	39.5	43.9	2715	7	US-11-096-051-2 Sequence 2, Appl
36	39.5	43.9	2721	7	US-11-096-051-10 Sequence 10, Appl
37	39.5	43.9	2725	7	US-11-096-051-8 Sequence 8, Appl
38	39	43.3	905	7	US-11-072-512-2728 Sequence 2728, Ap
39	38.5	42.8	1400	6	US-10-821-234-1045 Sequence 1045, Ap
40	38.5	42.8	1574	6	US-10-055-877-211 Sequence 211, App
41	38.5	42.8	2715	7	US-11-113-424-51 Sequence 51, Appl
42	38.5	42.8	3597	7	US-11-019-711-6 Sequence 6, Appl
43	38.5	42.8	3600	7	US-11-019-711-2 Sequence 2, Appl
44	38.5	42.8	3690	6	US-10-995-561-1016 Sequence 1016, Ap
45	38.5	42.8	3714	6	US-10-995-561-1015 Sequence 1015, Ap
46	38.5	42.8	3717	6	US-10-821-234-1076 Sequence 1076, Ap
47	38	42.2	27	6	US-10-895-861-30 Sequence 30, Appl
48	38	42.2	162	7	US-11-096-568A-9458 Sequence 9458, Ap
49	38	42.2	186	7	US-11-096-568A-9457 Sequence 9457, Ap
50	38	42.2	461	7	US-11-132-285-6 Sequence 6, Appl
51	38	42.2	461	7	US-11-182-946-4 Sequence 4, Appl
52	38	42.2	461	7	US-11-182-205-32 Sequence 32, Appl
53	38	42.2	627	6	US-10-330-773-78 Sequence 78, Appl
54	38	42.2	1683	7	US-11-131-479-38 Sequence 38, Appl
55	37.5	41.7	176	7	US-11-128-059-72 Sequence 72, Appl
56	37.5	41.7	232	7	US-11-128-059-66 Sequence 66, Appl
57	37.5	41.7	244	6	US-10-453-372-214 Sequence 214, App
58	37.5	41.7	315	6	US-10-453-372-212 Sequence 212, App
59	37.5	41.7	421	6	US-10-453-372-220 Sequence 220, App
60	37.5	41.7	533	6	US-10-453-372-230 Sequence 230, App
61	37.5	41.7	533	6	US-10-453-372-232 Sequence 232, App
62	37.5	41.7	539	7	US-11-183-136-38 Sequence 38, Appl
63	37.5	41.7	552	6	US-10-453-372-234 Sequence 234, App
64	37.5	41.7	552	6	US-10-453-372-246 Sequence 246, App
65	37.5	41.7	552	6	US-10-453-372-248 Sequence 248, App
66	37.5	41.7	552	6	US-10-453-372-250 Sequence 250, App
67	37.5	41.7	552	6	US-10-453-372-240 Sequence 240, App
68	37.5	41.7	552	6	US-10-453-372-242 Sequence 242, App
69	37.5	41.7	552	6	US-10-453-372-244 Sequence 244, App
70	37.5	41.7	552	6	US-10-453-372-248 Sequence 248, App
71	37.5	41.7	552	6	US-10-453-372-250 Sequence 250, App
72	37.5	41.7	556	6	US-10-453-372-210 Sequence 210, App
73	37.5	41.7	556	6	US-10-453-372-216 Sequence 216, App
74	37.5	41.7	669	6	US-10-453-372-218 Sequence 218, App
75	37.5	41.7	669	6	US-11-128-059-88 Sequence 88, Appl
76	37.5	41.7	721	7	US-10-453-372-208 Sequence 208, Appl
77	37.5	41.7	897	6	US-11-128-059-86 Sequence 86, Appl
78	37.5	41.7	931	7	US-11-128-059-86 Sequence 86, Appl
79	37.5	41.7	1198	6	US-10-453-372-880 Sequence 880, Appl
80	37.5	41.7	1327	7	US-11-128-059-92 Sequence 92, Appl
81	37.5	41.7	1327	7	US-11-128-059-84 Sequence 84, Appl
82	37.5	41.7	1398	6	US-10-055-877-46 Sequence 46, Appl
83	37.5	41.7	1398	6	US-10-453-372-872 Sequence 872, Appl
84	37.5	41.7	1403	6	US-10-055-877-52 Sequence 52, Appl
85	37.5	41.7	1403	6	US-10-453-372-878 Sequence 878, Appl
86	37.5	41.7	1404	6	US-10-055-877-44 Sequence 44, Appl
87	37.5	41.7	1404	6	US-10-453-372-870 Sequence 870, Appl
88	37.5	41.7	1416	6	US-11-128-059-4 Sequence 4, Appl
89	37.5	41.7	1418	6	US-10-453-372-864 Sequence 864, Appl
90	37.5	41.7	1450	6	US-10-055-877-48 Sequence 48, Appl
91	37.5	41.7	1450	6	US-10-453-372-874 Sequence 874, Appl
92	37.5	41.7	1502	6	US-10-453-372-252 Sequence 252, App
93	37.5	41.7	1510	6	US-10-453-372-254 Sequence 254, App
94	37.5	41.7	1547	6	US-10-453-372-886 Sequence 886, App
95	37.5	41.7	1577	6	US-10-055-877-54 Sequence 54, Appl
96	37.5	41.7	1577	6	US-10-453-372-882 Sequence 882, App
97	37.5	41.7	1577	6	US-10-453-372-884 Sequence 884, App
98	37.5	41.7	1594	6	US-10-453-372-860 Sequence 860, App

99 37.5 41.7 1609 7 US-11-072-175-185  
100 37.5 41.7 1616 6 US-10-821-234-1497

Sequence 185, App  
Sequence 1497, Ap

## ALIGNMENTS

RESULT 1  
US-10-878-556A-28

Sequence 28, Application US/10878556A  
Publication No. US2005026399A1  
GENERAL INFORMATION:  
APPLICANT: Hoffmann La-Roche Inc.  
TITLE OF INVENTION: HCV regulated protein expression  
FILE REFERENCE: 21762  
CURRENT APPLICATION NUMBER: US/10/878,556A  
NUMBER OF SEQ ID NOS: 199  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 28  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: sw\_hum/enol\_human  
DATABASE ENTRY DATE: 1995-02-01  
US-10-878-556A-28

Query Match 82.2% Score 74; DB 6; Length 458;  
Best Local Similarity 87.5% Pred. No. 0.00019;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 407 LVVGLCTGQIKTGPTC 422

RESULT 2

US-10-821-234-1553  
Sequence 1553, Application US/10821234  
Publication No. US2005025511A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Brigitte  
APPLICANT: Andaman, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pc\_seq\_genes Version 1.0  
SEQ ID NO 1553  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1553

Query Match 72.2% Score 65; DB 6; Length 434;  
Best Local Similarity 81.2% Pred. No. 0.0049;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 384 LVVGLCTGQIKTGAPC 399

RESULT 3

US-11-168-637-10  
Sequence 10, Application US/11168637  
Publication No. US2006005174A1

GENERAL INFORMATION:  
APPLICANT: Austen, Kimberly M.  
APPLICANT: Kapil, Sanjay  
APPLICANT: Kim, Jeong-Ki

TITLE OF INVENTION: FELINE INFECTIOUS PERITONITIS (FIP) AND  
SYSTEMIC MULTI-ORGAN CORONAVIRUS BIOMARKERS AND SCREENING  
METHODS  
FILE REFERENCE: 14337-005001  
CURRENT APPLICATION NUMBER: US/11/168,637  
CURRENT FILING DATE: 2005-06-28  
PRIOR APPLICATION NUMBER: US 60/656,027  
PRIOR FILING DATE: 2005-02-24  
PRIOR APPLICATION NUMBER: US 60/584,439  
PRIOR FILING DATE: 2004-06-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Felis cattus  
US-11-168-637-10

Query Match 72.2% Score 65; DB 7; Length 434;  
Best Local Similarity 81.2% Pred. No. 0.0049;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 384 LVVGLCTGQIKTGAPC 399

RESULT 4

US-10-055-877-213  
Sequence 213, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: Decristofaro, Marc  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spyrek, Kimberly  
APPLICANT: Patel, Luca  
APPLICANT: Kekuda, Rameen  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zernusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Burgess, Catherine  
APPLICANT: Paturajan, Meera  
APPLICANT: Eiben, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier, Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stacie  
APPLICANT: Boldog, Ferenc  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23

```

; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 213
; LENGTH: 1620
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-055-877-213

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Query Match      52.8%; Score 47.5; DB 6; Length 1620;
Best Local Similarity 62.5%; Pred. No. 9.2;
Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      2 VVGLCTC-QIKTGPAC 16
Db      876 VTGTCTCLPGKTGPLC 891

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RESULT 5
; Sequence 212, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patcurajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkov, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corinne
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892

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; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 1664
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-055-877-212

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Query Match      52.8%; Score 47.5; DB 6; Length 1664;
Best Local Similarity 62.5%; Pred. No. 9.4;
Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      2 VVGLCTC-QIKTGPAC 16
Db      828 VTGTCTCLPGKTGPLC 843

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RESULT 6
; Sequence 111, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-068-783-111

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Query Match      51.1%; Score 46; DB 7; Length 46;
Best Local Similarity 53.8%; Pred. No. 0.67;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      4 GLCTCQIKTGPAC 16
Db      28 GACRCKITSPKC 40

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RESULT 7
US-11-172-740-2156
; Sequence 2156, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:

```

```
/ APPLICANT: MASCIA, Peter
/ APPLICANT: ALEXANDROV, Nikolai
/ APPLICANT: BROVER, Vvachestlav
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
/ TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
/ FILE REFERENCE: 2750-1602PUS2
/ CURRENT APPLICATION NUMBER: US/11/172,740
/ CURRENT FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: 60/583,621
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/584,829
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/584,800
/ PRIOR FILING DATE: 2004-06-30
/ NUMBER OF SEQ ID NOS: 2523
/ SEQ ID NO 2156
/ LENGTH: 127
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)-(127)
/ OTHER INFORMATION: Public GI no. 46396244
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making smaller plants
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making stronger plants
/ US-11-172-740-2156

Query Match      50.6%; Score 45.5; DB 7; Length 127;
Best Local Similarity 47.4%; Pred. No. 2;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY      3  VGLC-----TCQIKTGPA 16
Db      33  LGLCETCDERCQAHGFGSC 51

RESULT 8
US-11-043-693-51
/ Sequence 51, Application US/11043693
/ Publication No. US20050281831A1
/ GENERAL INFORMATION:
/ APPLICANT: Davis-Smyth, Terri L.
/ APPLICANT: Chen, Helen H.
/ APPLICANT: Presta, Leonardo
/ APPLICANT: Ferrara, Napoleone
/ TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
/ TITLE OF INVENTION: PRODUCTION
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Dorsey & Whitney LLP
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/043,693
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/ FILING DATE: 26-Jan-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/105,901
/ FILING DATE: 20-Mar-2002
/ APPLICATION NUMBER: 09/348,886
/ FILING DATE: 01-JUL-1999
/ APPLICATION NUMBER: US 08/643,839
/ FILING DATE: 07-MAY-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Richard F. Trecartin
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 100 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-11-043-693-51

Query Match      47.8%; Score 43; DB 7; Length 100;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4  GLCTCQIKTGPA 15
Db      192  GLYTCRVRSGPS 203

RESULT 10
US-11-016-503-8
/ Sequence 8, Application US/11016503
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```
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-8

Query Match          47.8%; Score 43; DB 7; Length 462;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 202 GLYTCRVRSGPS 213

RESULT 11
US-11-016-503-4
; Sequence 4, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-4

Query Match          47.8%; Score 43; DB 7; Length 557;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 297 GLYTCRVRSGPS 308

RESULT 12
US-11-016-503-2
; Sequence 2, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
```

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; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-2

Query Match          47.8%; Score 43; DB 7; Length 567;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 307 GLYTCRVRSGPS 318

RESULT 13
US-11-016-503-10
; Sequence 10, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-10

Query Match          47.8%; Score 43; DB 7; Length 567;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 307 GLYTCRVRSGPS 318

RESULT 14
US-11-043-693-1
; Sequence 1, Application US/11043693
; Publication No. US20050281831A1
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; APPLICANT: Ferrara, Napoleone
```

```
/ TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
/ TITLE OF INVENTION: PRODUCTION
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Dorey & Whitney LLP
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/043,693
/ FILING DATE: 26-Jan-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/105,901
/ FILING DATE: 20-Mar-2002
/ APPLICATION NUMBER: 09/348,886
/ FILING DATE: 01-JUL-1999
/ APPLICATION NUMBER: US 08/643,839
/ FILING DATE: 07-MAY-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Richard F. Trecartin
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NEC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 758 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-11-043-693-1

Query Match      47.8%; Score 43; DB 7; Length 758;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
Db      307 GLYTCRVRSGPS 318

RESULT 15
US-10-821-234-1622
/ Sequence 1622, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Scache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1622
/ LENGTH: 1338
/ TYPE: PRT
```

```
/ ORGANISM: Homo sapiens
/ US-10-821-234-1622

Query Match      47.8%; Score 43; DB 6; Length 1338;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
Db      307 GLYTCRVRSGPS 318

RESULT 16
US-11-109-156-23
/ Sequence 23, Application US/1109156
/ Publication No. US20050250144A1
/ GENERAL INFORMATION:
/ APPLICANT: Toshio Ota
/ APPLICANT: Takao Isogai
/ APPLICANT: Tetsuo Nishikawa
/ APPLICANT: Koji Hayashi
/ APPLICANT: Kaoru Otsuka
/ APPLICANT: Jun-ichi Yamamoto
/ APPLICANT: Shizuko Ishii
/ APPLICANT: Tomoyasu Sugiyama
/ APPLICANT: Ai Wakamatsu
/ APPLICANT: Keiichi Nagai
/ APPLICANT: Tetsuji Otsubki
/ APPLICANT: Shin-ichi Funahashi
/ APPLICANT: Chiaki Senoo
/ APPLICANT: Jun-ichi Nezu
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
/ FILE REFERENCE: 06501-099002
/ CURRENT APPLICATION NUMBER: US/11/109,156
/ PRIOR FILING DATE: 2005-04-19
/ PRIOR APPLICATION NUMBER: US/10/060,065
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP00/05061
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/159,590
/ PRIOR FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US 60/183,322
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: JP 11-248036
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: JP 2000-118776
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: JP 2000-183767
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: JP 2000-241899
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 23
/ LENGTH: 1338
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-109-156-23

Query Match      47.8%; Score 43; DB 7; Length 1338;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
Db      307 GLYTCRVRSGPS 318

RESULT 17
US-11-075-047A-2
/ Sequence 2, Application US/11075047A
/ Publication No. US2006030000A1
```



GENERAL INFORMATION:  
APPLICANT: ALITALO, et al.  
TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS  
FILE REFERENCE: 28967/39700A  
CURRENT APPLICATION NUMBER: US/11/075,047A  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/550,907  
PRIOR FILING DATE: 2004-03-07  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 1338  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-075-047A-2

Query Match 47.8%; Score 43; DB 7; Length 1338;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
DB 307 GLYTCTCRSGPS 318

RESULT 18  
US-11-043-693-33  
Sequence 33, Application US/11043693  
Publication No. US20050281831A1  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dorsey & Whitney LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/043,693  
FILING DATE: 26-Jan-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/105,901  
FILING DATE: 20-Mar-2002  
APPLICATION NUMBER: 09/348,886  
FILING DATE: 01-JUL-1999  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard F. Treacartn  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1362 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-11-043-693-33

Query Match 47.8%; Score 43; DB 7; Length 1362;  
Best Local Similarity 50.0%; Pred. No. 41;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15  
DB 305 GLYTCTCRSGPS 316

RESULT 19  
US-11-182-343-31  
Sequence 31, Application US/11182343  
Publication No. US20060018910A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce  
APPLICANT: Galbeto, Antonio  
APPLICANT: Melvin, Carlie  
APPLICANT: Roberts, Luisa M.  
TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER  
FILE REFERENCE: PC32226A  
CURRENT APPLICATION NUMBER: US/11/182,343  
CURRENT FILING DATE: 2005-07-15  
PRIOR APPLICATION NUMBER: 60/588,721  
PRIOR FILING DATE: 2004-07-16  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 31  
LENGTH: 296  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-182-343-31

Query Match 46.7%; Score 42; DB 7; Length 296;  
Best Local Similarity 53.8%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 16  
DB 56 GACTCTCCCTGTGC 68

RESULT 20  
US-11-112-240-1  
Sequence 1, Application US/11112240  
Publication No. US20050287140A1  
GENERAL INFORMATION:  
APPLICANT: Smothers, James F.  
APPLICANT: Fanelow III, William C.  
APPLICANT: Kariv, Revital  
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
FILE REFERENCE: A-953A(US)  
CURRENT APPLICATION NUMBER: US/11/112,240  
CURRENT FILING DATE: 2005-04-21  
PRIOR APPLICATION NUMBER: US 60/564,885  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/585,885  
PRIOR FILING DATE: 2004-07-06  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-112-240-1

Query Match 46.7%; Score 42; DB 7; Length 360;  
Best Local Similarity 53.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPAK 16  
Db 56 GACTCTCCTGTGC 68

## RESULT 21

US-11-112-304A-1  
; Sequence 1, Application US/11112304A  
; Publication No. US2006002931A1  
; GENERAL INFORMATION:  
; APPLICANT: AMGEN, INC.  
; APPLICANT: AMGEN, INC.  
; APPLICANT: Smothers, James  
; APPLICANT: Farnlow III, William C.  
; APPLICANT: Kariv, Revital  
; TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
; FILE REFERENCE: 3447  
; CURRENT APPLICATION NUMBER: US/11/112,304A  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/565,158  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/564,885  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/571,566  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/585,686  
; PRIOR FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-112-304A-1

Query Match 46.7%; Score 42; DB 7; Length 360;  
Best Local Similarity 53.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKTGPAK 16  
Db 56 GACTCTCCTGTGC 68

RESULT 22  
US-10-980-388-40  
; Sequence 40, Application US/10980388  
; Publication No. US2005025490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl  
; FILE REFERENCE: 00325.US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,397  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,247

; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/217,369  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/217,370  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/218,492  
; PRIOR FILING DATE: 2000-07-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-388-40

Query Match 46.7%; Score 42; DB 6; Length 544;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 4 GLCTCQIKTGPAK 16  
Db 276 GCTCTCAGCTAC 288

RESULT 23  
US-11-096-568A-24462  
; Sequence 24462, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 24462  
; LENGTH: 839  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(839)  
; OTHER INFORMATION: Ceres Seq. ID no. 12435290  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (325)..(325)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24462

Query Match 45.6%; Score 41; DB 7; Length 839;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKT 12  
Db 437 LVAGLCTCAVKT 448

RESULT 24  
US-11-096-568A-24461  
; Sequence 24461, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO: 24461  
LENGTH: 878  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(878)  
OTHER INFORMATION: Ceres Seq. ID no. 12435289  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (364)..(364)  
OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24461

Query Match  
Best Local Similarity 45.6%; Score 41; DB 7; Length 878;  
Best Local Similarity 50.0%; Pred. No. 57;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTCOIKT 12  
Db 476 LLAGLCTCAVRT 487

RESULT 25  
US-11-096-568A-24460  
Sequence 24460, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nikolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592US2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 24460  
LENGTH: 909  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(909)  
OTHER INFORMATION: Ceres Seq. ID no. 12435288  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (395)..(395)  
OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24460

Query Match  
Best Local Similarity 45.6%; Score 41; DB 7; Length 909;  
Best Local Similarity 50.0%; Pred. No. 59;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTCOIKT 12  
Db 507 LLAGLCTCAVRT 518

RESULT 26  
US-11-114-962-1  
Sequence 1, Application US/11114962  
Publication No. US20060030694A1  
GENERAL INFORMATION:  
APPLICANT: Kitajewski, Jan  
APPLICANT: Shawber, Carrie  
TITLE OF INVENTION: Notch-Based Fusion Proteins and Uses Thereof  
FILE REFERENCE: 0575/71308-A  
CURRENT APPLICATION NUMBER: US/11/114,962  
CURRENT FILING DATE: 2005-04-26  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 1  
LENGTH: 1433  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-11-114-962-1

Query Match  
Best Local Similarity 45.0%; Score 40.5; DB 7; Length 1433;  
Best Local Similarity 61.5%; Pred. No. 11e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Oy 5 ICTCG-QIKTGPAC 16  
Db 397 ICTCPRGYTGAPAC 409

RESULT 27  
US-11-050-346-67  
Sequence 67, Application US/11050346  
Publication No. US2006002924A1  
GENERAL INFORMATION:  
APPLICANT: BODMER, MARK WILLIAM  
APPLICANT: CHAMPION, BRIAN ROBERT  
APPLICANT: LENNARD, ANDREW CHRISTOPHER  
APPLICANT: MCKENZIE, GRAHAME JAMES  
APPLICANT: TUGAL, TAMARA  
APPLICANT: WARD, GEORGE ALBERT  
TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALING PATHWAY MODULATORS AND  
FILE REFERENCE: 674525-2016  
CURRENT APPLICATION NUMBER: US/11/050,346  
CURRENT FILING DATE: 2005-02-03  
PRIOR APPLICATION NUMBER: GB 0312062.3  
PRIOR FILING DATE: 2003-05-24  
PRIOR APPLICATION NUMBER: PCT/GB03/01525  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: GB 0300234.2  
PRIOR FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: GB 0218068.5  
PRIOR FILING DATE: 2002-08-03  
PRIOR APPLICATION NUMBER: GB 0220849.4  
PRIOR FILING DATE: 2002-09-07  
PRIOR APPLICATION NUMBER: GB 0220912.0  
PRIOR FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: GB 0220913.8  
PRIOR FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: PCT/GB02/05137  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: PCT/GB02/05133  
PRIOR FILING DATE: 2002-11-13  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 67  
LENGTH: 2556  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (891)  
OTHER INFORMATION: Variable amino acid  
US-11-050-346-67

Query Match  
Best Local Similarity 45.0%; Score 40.5; DB 7; Length 2556;  
Best Local Similarity 61.5%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Oy 5 ICTCG-QIKTGPAC 16  
Db 397 ICTCPRGYTGAPAC 409

RESULT 28  
US-10-793-626-2510  
Sequence 2510, Application US/10793626

```

; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STRAPHILOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS4800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2510
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (205)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2510

```

```

Query Match      44.4%; Score 40; DB 6; Length 205;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 GLCTCQIKTG 13
Db      141 GLCTCDVSTG 150

```

```

RESULT 29
US-10-894-592-3
; Sequence 3, Application US/10894592
; Publication No. US20060019335A1
; GENERAL INFORMATION:
; APPLICANT: Du, Chunying
; TITLE OF INVENTION: Compositions and Methods to Promote c-IAP Autodegradation
; FILE REFERENCE: 68175
; CURRENT APPLICATION NUMBER: US/10/894,592
; CURRENT FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-894-592-3

```

```

Query Match      44.4%; Score 40; DB 6; Length 1356;
Best Local Similarity 53.8%; Pred. No. 12e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      4 GLCTCQIKTG 16
Db      893 GCCTCTGTGTGTC 905

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RESULT 30
US-11-096-051-12
; Sequence 12, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vermet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967

```

```

; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-12

```

```

Query Match      43.9%; Score 39.5; DB 7; Length 257;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 8; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

```

```

QY      4 GLCTCQIK-TGPAC 16
Db      177 GTCRCCEGWTGPAC 190

```

```

Search completed: April 3, 2006, 08:07:30
Job time : 13 secs

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